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WEST[Generate Collection](#)[Print](#)**Search Results - Record(s) 1 through 4 of 4 returned.**☐ 1. Document ID: US 6228983 B1

L3: Entry 1 of 4

File: USPT

May 8, 2001

US-PAT-NO: 6228983

DOCUMENT-IDENTIFIER: US 6228983 B1

**** See image for Certificate of Correction ****

TITLE: Human respiratory syncytial virus peptides with antifusogenic and antiviral activities

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw Desc	Image
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☐ 2. Document ID: US 6093794 A

L3: Entry 2 of 4

File: USPT

Jul 25, 2000

US-PAT-NO: 6093794

DOCUMENT-IDENTIFIER: US 6093794 A

TITLE: Isolated peptides derived from the Epstein-Barr virus containing fusion inhibitory domains

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw Desc	Image
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☐ 3. Document ID: US 6060065 A

L3: Entry 3 of 4

File: USPT

May 9, 2000

US-PAT-NO: 6060065

DOCUMENT-IDENTIFIER: US 6060065 A

TITLE: Compositions for inhibition of membrane fusion-associated events, including influenza virus transmission

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw Desc	Image
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☐ 4. Document ID: US 5871730 A

L3: Entry 4 of 4

File: USPT

Feb 16, 1999

US-PAT-NO: 5871730

DOCUMENT-IDENTIFIER: US 5871730 A

TITLE: Thermostable xylanase DNA, protein and methods of use

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Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	RMC	Draw Desc	Image
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Terms	Documents
L2 same (position 116 or position 118 or 116 or 118)	4

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FILE 'CAPLUS, BIOSIS, SCISEARCH, BIOTECHDS, DGENE, PASCAL, CABA, LIFESCI,
BIOTECHNO, AGRICOLA, EMBASE, GENBANK, MEDLINE, ESBIODASE, FSTA' ENTERED
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L2 2233 S L1 AND (VARIANT OR MUTANT)
L3 2880 S L1 AND (VARIAN? OR MUTA?)
L4 33 S L3 AND (POSITION 116 OR POSITION 118 OR 116 OR 118)
L5 0 S L1 AND (POSITION 11 OR 11D)
L6 4 S L1 AND (POSITION 144R OR POSITION 144 OR POSITION 161R OR 161
L7 21 DUP REM L4 (12 DUPLICATES REMOVED)
L8 21 DUP REM L4 (12 DUPLICATES REMOVED)
L9 4 DUP REM L6 (0 DUPLICATES REMOVED)

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L9 ANSWER 1 OF 4 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI

ACCESSION NUMBER: 2003-01501 BIOTECHDS

TITLE: Bleaching of chemical pulp involves, exposing chemical pulp to acidic bleaching stage to produce partially bleached pulp and treating with thermophilic, alkalophilic **xylanase** in alkaline extraction stage at preset condition; pulp bleaching using recombinant enzyme

AUTHOR: TOLAN J; POPOVICI C; FOODY P J

PATENT ASSIGNEE: IOGEN BIO PROD CORP

PATENT INFO: WO 2002052100 4 Jul 2002

APPLICATION INFO: WO 2001-CA1837 19 Dec 2001

PRIORITY INFO: US 2000-258163 22 Dec 2000; US 2000-258163 22 Dec 2000

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: WPI: 2002-599582 [64]

AB DERWENT ABSTRACT:

NOVELTY - A chemical pulp is bleached by exposing pulp to an acidic bleaching stage to produce a partially bleached pulp and treating with a thermophilic, alkalophilic **xylanase** in an alkaline extraction stage with a final pH of 8-14.

BIOTECHNOLOGY - Preferred Enzyme: The thermophilic, alkalophilic **xylanase** comprises a genetically modified **xylanase**, comprising a family 11 **xylanase** from *Trichoderma*. The **xylanase** is a genetically modified *Trichoderma reesei*, selected from Trx HML 75A, 105H, 125A, 129E, 132R, 135R, 144R, 157D, 161R, 162H, 165H; TrxHML 75A, 105H, 125A, 135R, 144R, 157D, 161R, 162H, 165H; TrxHML 75A, 105H, 125A, 129E; and TrxHML 75A, 105H, 125A, 129E, 135R, 144R, 157D, 161R, 162H, 165H (each sequence having 190 amino acids given in the specification), where HML denotes the mutations 10H, 27M and 29L. The **xylanase** comprises BioBrite **xylanase** or a wild type **xylanase**. Preferred Method: The alkaline extraction is performed at 60-120degreesC at a final pH of 9-11.5 for 30-120 minutes. The alkaline extraction is performed using oxygen and/or hydrogen peroxide. 0.1-10 kg of oxygen and hydrogen peroxide is present per ton of pulp. The partially bleached pulp is treated with a second **xylanase** at pH 8-14. The second **xylanase** is identical to the first **xylanase**. The pulp is treated with the first **xylanase** after alkaline oxygen delignification stage. The enzymatic treatment is performed in condition different from the alkaline extraction stage. Alternately, the chemical pulp is exposed to a chemical bleaching stage to produce a partially bleached pulp. The partially bleached pulp is incubated with an extraction filtrate containing the **xylanase** and subsequently washed with water to produce a papricycle washed **xylanase** treated pulp. The papricycle pulp is treated with the **xylanase** at a final pH of 8-14. Then the extraction filtrate is removed from the extract.

USE - For bleaching pulp using **xylanase**.

ADVANTAGE - The method enables to ensure proper mixing of the enzyme with pulp, to control and monitor process conditions such as pH, temperature, enzyme dosage and incubation time. The method does not necessarily require significant changes to existing pulp bleaching equipment, such as purchasing and implementing costly vessels for performing **xylanase** treatment. By carrying out **xylanase** treatment in an alkaline extraction stage, little or no acid is required to adjust the pH of the pulp prior to **xylanase** addition. The reduction or elimination of acid reduces corrosion of mill equipment and the costs associated with a pulp bleaching process. The addition of **xylanase** after an acidic bleaching stage, or before and after a bleaching stage increases the overall effect of enzyme treatment. The pulp bleaching method also reduce the amount of chemicals required to bleach pulp and also reduce the amount of chlorinated effluent waste

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produced by a pulp bleaching process.

EXAMPLE - Unbleached hardwood kraft pulp was incubated at 60 degrees C, at initial pH 9.4 for 60 minutes to simulate the conditions of an enzyme treatment stage. The pulp was washed with water. 15 g of sample of pulp was subjected to chlorine dioxide bleaching stage. Chlorine dioxide was added to the pulp and the system was maintained in a heat-sealable plastic bag. The pulp mixture was cooled to 4 degrees C to minimize evaporation. The kappa factor was recommended to be about 0.17 to avoid formation of furans and dioxins. The pulp was adjusted to a 10% consistency with tap water and the initial pH was adjusted to 9.4 with sodium hydroxide. The pulp was heated to 60degreesC and a genetically modified *Trichoderma reesei* **xylanase** (having Trx HML 75A, 105H, 125A, 129E, 132R, 135R, 144R, 157D, 161R, 162H, 165H at amount of 2.0 units/g of pulp with the enzyme stock at 33 units/ml was added to the pulp. Pulp was treated in a similar manner but with a thermophilic, alkalophilic, **xylanase** in the alkaline extraction stage and exhibited a kappa number of 4.8. (61 pages)

L9 ANSWER 2 OF 4 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI

ACCESSION NUMBER: 2002-09767 BIOTECHDS

TITLE: Modified **xylanase** exhibiting increased
thermostability and alkalophilicity useful for industrial
processing e.g. for pulp manufacturing;
vector-mediated gene transfer and expression in host cell
for recombinant protein production and feedstuff
manufacture

AUTHOR: SUNG W L

PATENT ASSIGNEE: NAT RES COUNCIL CANADA

PATENT INFO: WO 2001092487 6 Dec 2001

APPLICATION INFO: WO:2000:CA769 31 May 2000

PRIORITY INFO: US 2000-213803 31 May 2000

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: WPI: 2002-171435 [22]

AB DERWENT ABSTRACT:

NOVELTY - A modified **xylanase** (I) exhibiting increased
thermostability and alkalophilicity, comprises at least one substituted
amino acid residue at position 75, 104, 105, 125, 129, 132, 135, 144,
157, 161, 162 or 165, where the position is determined from sequence
alignment of (I) with a 190 residue *Trichoderma reesei* **xylanase**
II amino acid sequence (S1), fully defined in the specification, is new.

DETAILED DESCRIPTION - A modified **xylanase** (I) exhibiting
increased thermostability and alkalophilicity, comprises at least one
substituted amino acid residue at position 75, 104, 105, 125, 129, 132,
135, 144, 157, 161, 162 or 165, where the position is determined from
sequence alignment of (I) with a 190 residue *Trichoderma reesei*
xylanase II amino acid sequence (S1), fully defined in the
specification, is new. (I) is characterized as having a maximum effective
temperature (MET) of 69-78 degrees C, and maximum effective pH (MEP) of
5.8-7.6, where (I) is a family 11 **xylanase** obtained from a
Trichoderma sp..

BIOTECHNOLOGY - Preferred Variant: (I) exhibits improved
thermophilicity and/or alkalophilicity, in comparison to a corresponding
native **xylanase**. The substituted amino acid is at position 75
and is selected from non-polar and a polar amino acid e.g. Ala, Cys, Gly
and Thr. (I) is derived from a family 11 **xylanase** e.g. *T.reesei*
xylanase. (I) further comprises a His at position 10, Met at
position 27 and Leu at position 29 (HML). (I) comprises at least one
substituted polar amino acid residue at position 105, e.g. His, Lys and
Arg. (I) further comprises a second substituted non-polar or polar amino
acid residue at position 75. The polar amino acids at **positions**
161, 162 and 165 are selected from Arg, Lys and His, and the
polar amino acid at position 157 is selected from Asp and Glu. (I)
further comprises at least one substituted non-polar amino acid, Ala, at

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position 125, and a second substituted acidic amino acid, Glu, at position 129. (I) further comprises a third substituted non-polar amino acid residue (Ala, Cys, Gly and Thr), at position 75, and a fourth substituted polar amino acid residue (His, Lys, and Arg) at position 105. A fifth substituted non-polar amino acid residue, Pro, is present at position 104. Fifth-eleventh substituted polar amino acid residues at positions 132, 135, 144, 157, 161, 162 and 165 are also provided. The MET is 70-75 degrees C, and The pH of MEP is 6.5-7.4. (I) is further characterized as having a maximum effective pH (MEP) is 5.8-7.6. (I) is preferably selected from TrX-161R-162H-165H; TrX-HML-75A; TrX-HML-105H; TrX-HML-105R; TrX-HML-105K; TrX-HML-75A-105H; TrX-HML-75A-105R; TrX-HML-75C-105R; TrX-HML-75G-105R; TrX-HML-75T-105R; TrX-HML-125A; TrX-HML-125A-129E; TrX-HML-75G-105R-125A-129E (TrX-HML-GRAE); TrX-HML-75A-105H-125A-129E (TrX-HML-AHAE); TrX-HML-75G-105H-125A-129E (TrX-HML-GHAE); TrX-HML-75A-105R-125A-129E (TrX-HML-ARAE); TrX-HML-75G-104P-105R-125A-129E (TrX-HML-GPRAE); TrX-HML-75G-104P-105H-125A-129E (TrX-HML-GPHAE); TrX-HML-AHAE-RR; TrX-HML-AHAE-RRR; TrX-HML-AHAE-RRR-DRHH; TrX-HML-AHA-RR-DRHH; and TrX-HML-AHAE-RR-DRHH.

USE - (I) is useful in industrial process such as pulp manufacturing (claimed). (I) is also useful for bleaching of pulp, processing of precision devices and improving digestibility of poultry and swine feed.

ADVANTAGE - (I) has improved performance at conditions of high temperature and pH, and exhibits improved thermophilicity and/or alkalophilicity in comparison to a corresponding native **xylanase**

EXAMPLE - For the construction of TrX(92-190), ten overlapping oligonucleotides XyTv-101, XyTv-102, TrX-103, XyTv-104, XyTv-105, XyTv-106, XyTv-107, TrX-108, XyTv-109, XyTv-110, were designed with codon usage frequency imitating that of *Escherichia coli*. The *SalI* and *BglII* cohesive ends of two terminal oligonucleotides enabled the enzymatic ligation of the ten fragments into the linearized plasmid pXYbc. The ten oligonucleotides encoding the TrX(92-190) region of *Trichoderma xylanase* were phosphorylated in a mixture containing 10X standard kinase buffer (0.4 micro-L), 1 mM ATP (4 micro-L), T4 DNA kinase (5 units), and water (3 micro-L). Phosphorylation reactions were carried out for 1 hour at 37 degrees C. The solutions were then combined and heated to 70 degrees C for 10 minutes. After being cooled slowly to room temperature, the combined solutions were added to a mixture of 4 mM ATP (3.5 micro-L), *EcoRI-HindIII* linearized plasmid pUC119 and T4 DNA ligase (3.5 micro-L), and incubated at 12 degrees C for 20 hours. Aliquots of the ligation mixture were used to transform *E. coli* HB101 on YT plates containing ampicillin (100 mg/L). For the preparation of a hybridization probe, one of the oligonucleotides, e.g. XyTv-110 (1 micro-L) was phosphorylated with 32P-ATP (3 micro-L) using T4 DNA kinase (1 micro-L), 10X kinase buffer (1 micro-L), and water (4 micro-L) at 37 degrees C for 1 hour. Transformants were selected randomly for hybridization analysis. Colonies were grown on YT plates with ampicillin overnight, and transferred onto nylon filters. They were then denatured and neutralized. After ultraviolet irradiation at 254 nm for 8 minutes, the filters were washed with 6X saline sodium chloride (SSC)-0.05 % Triton X-100 for 30 minutes. Positively hybridized clones with the intermediate plasmid pBcX-TrX were identified by auto-radiographic analysis. (109 pages)

L9 ANSWER 3 OF 4 DGENE (C) 2003 THOMSON DERWENT

ACCESSION NUMBER: AAE18496 Protein DGENE

TITLE: Modified **xylanase** exhibiting increased thermostability and alkalophilicity useful for industrial processing e.g. for pulp manufacturing -

INVENTOR: Sung W L

PATENT ASSIGNEE: (CAN)NAT RES COUNCIL CANADA.

PATENT INFO: WO 2001092487 A2 20011206

109p

APPLICATION INFO: WO 2001-CA769 20010531

PRIORITY INFO: US 2000-213803P 20000531

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DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 2002-171435 [22]
DESCRIPTION: Trichoderma reesei **xylanase** mutant, TrX-157D-161R-162H-165H.

AB The present invention relates to a modified **xylanase** exhibiting increased thermostability and alkalophilicity. Modified **xylanase** is useful in industrial process such as pulp manufacturing. Modified **xylanase** is also useful for bleaching of pulp, processing of precision devices and improving digestibility of poultry and swine feed. Modified **xylanase** has improved performance at conditions of high temperature and pH and exhibits improved thermophilicity and/or alkalophilicity in comparison to corresponding native **xylanase**. The present sequence is Trichoderma reesei **xylanase** (TrX) mutant. Note: The present sequence is not shown in the specification but is derived from wild type **xylanase** referred as SEQ ID NO: 16 (AAE18452) and shown in page 80-81 of the specification.

L9 ANSWER 4 OF 4 DGENE (C) 2003 THOMSON DERWENT

ACCESSION NUMBER: AAE18495 Protein DGENE
TITLE: Modified **xylanase** exhibiting increased thermostability and alkalophilicity useful for industrial processing e.g. for pulp manufacturing -
INVENTOR: Sung W L
PATENT ASSIGNEE: (CANA)NAT RES COUNCIL CANADA.
PATENT INFO: WO 2001092487 A2 20011206 109p
APPLICATION INFO: WO 2001-CA769 20010531
PRIORITY INFO: US 2000-213803P 20000531
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 2002-171435 [22]
DESCRIPTION: Trichoderma reesei **xylanase** mutant, TrX-161R-162H-165H.

AB The present invention relates to a modified **xylanase** exhibiting increased thermostability and alkalophilicity. Modified **xylanase** is useful in industrial process such as pulp manufacturing. Modified **xylanase** is also useful for bleaching of pulp, processing of precision devices and improving digestibility of poultry and swine feed. Modified **xylanase** has improved performance at conditions of high temperature and pH and exhibits improved thermophilicity and/or alkalophilicity in comparison to corresponding native **xylanase**. The present sequence is Trichoderma reesei **xylanase** (TrX) mutant. Note: The present sequence is not shown in the specification but is derived from wild type **xylanase** referred as SEQ ID NO: 16 (AAE18452) and shown in page 80-81 of the specification.

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L3 18 S L2 AND (POSITION 116 OR POSITION 118 OR 116 OR 118)
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L4 ANSWER 1 OF 6 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2003:434726 CAPLUS
TITLE: Trichoderma reesei **xylanase** II enzymes with enhanced thermophilicity and alkalophilicity
INVENTOR(S): Sung, Wing L.
PATENT ASSIGNEE(S): National Research Council of Canada, Can.
SOURCE: PCT Int. Appl., 105 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003046169	A2	20030605	WO 2002-CA1758	20021120
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.: US 2001-990874 A 20011121

AB The present invention provides a **xylanase**, or a modified **xylanase** enzyme comprising at least one substituted amino acid residue at a position selected from the group consisting of amino acid 11, 116, 118, 144 and 161, the position detd. from sequence alignment of the modified **xylanase** with Trichoderma reesei **xylanase** II amino acid sequence. The **xylanases** described herein exhibit improved thermophilicity, alkalophilicity, expression efficiency, or a combination thereof, in comparison to a corresponding native **xylanase**. The max. effect temp. is 69-84.degree. and the max effective pH is 5.8-8.4. The improved properties of **xylanase** II muteins are of use in industrial processes, such as paper pulp manuf.

L4 ANSWER 2 OF 6 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI

ACCESSION NUMBER: 2003-01486 BIOTECHDS
TITLE: Novel **xylanase** activity protein, useful in bleaching process of pulp and in food and animal feed industry, has enhanced thermostability and alkalophilicity; recombinant enzyme production via plasmid expression useful for animal feedstuff
AUTHOR: BENTZIEN J; DAHIYAT B
PATENT ASSIGNEE: XENCOR INC
PATENT INFO: WO 2002038746 16 May 2002
APPLICATION INFO: WO 2001-US48018 9 Nov 2001
PRIORITY INFO: US 2000-710050 10 Nov 2000; US 2000-710050 10 Nov 2000
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2002-608200 [65]

AB DERWENT ABSTRACT:

NOVELTY - A non-naturally occurring **xylanase** activity (XA) protein (I) comprising an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans **xylanase**, where the protein has been modified to exhibit enhanced thermophilicity, alkalophilicity, or thermostability relative to naturally occurring

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B.circulans **xylanase**, and has at least 5 amino acid substitutions, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for: (1) a recombinant nucleic acid (II) encoding (I); (2) an expression vector (III) comprising (II); (3) a host cell (IV) comprising (II) or (III); (4) producing (I); (5) a non-naturally occurring XA conformer (V) having a three dimensional backbone structure that substantially corresponds to the three dimensional backbone structure of B.circulans **xylanase**, where the amino acid sequence of the conformer and the amino acid sequence of the B.circulans **xylanase** are less than about 97% identical; (6) a bleaching agent (VI) comprising (I) as an active ingredient; (7) a non-naturally occurring XA amino acid sequence selected from a group as given in the specification; (8) a non-naturally occurring XA nucleic acid sequence selected from a group as given in the specification; and (9) a XA library comprising **variants** of XA, where the **variants** have been altered to exhibit enhanced alkalophilicity, thermophilicity, or thermostability relative to a naturally occurring B.circulans **xylanase**.

WIDER DISCLOSURE - **Variants** of (I) are also disclosed.

BIOTECHNOLOGY - Preparation: (I) is prepared by culturing (IV) under conditions suitable for the expression of (II) and recovering the expressed XA protein. Preferred Protein: (I) comprises at least three amino acid substitutions at positions chosen from 5, 7, 11, 26, 28, 30, 37, 39, 53, 58, 63, 64, 65, 67, 79, 80, 83, 84, 85, 88, 96, 98, 100, 102, 103, 105, 109, 110, 115, 118, 125, 128, 129, 130, 132, 136, 142, 144, 147, 148, 149, 150, 152, 156, 158, 160, 167, 168, 171, 176, 180, and 182. In (V), at least 90% or 100% of the non-identical amino acids are in the core region of the conformer.

USE - A bleaching agent comprising (I) is useful for bleaching pulp, by contacting pulp with the bleaching agent, which further comprises chemical bleaching and/or an alkali extraction before, after or during contacting pulp with the bleaching agent (claimed). XA proteins and nucleic acids are useful in the bioconversion of lignocellulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g., improving the quality of dough, help bread rise and processing of wheat and corn for starch production, use as animal food additives to aid in the digestibility of feedstuffs and in the washing of super precision devices and semiconductors.

ADVANTAGE - (I) is more alkalophilic, thermophilic and thermostable and hydrolyzes a substrate more efficiently than B.circulans **xylanase**.

EXAMPLE - Sequences for novel thermostable, thermophilic and/or alkaliphilic **xylanase** activity (XA) proteins were designed by optimizing residues in the core of the protein, residues around D83, residues around the helix region, and residues around the active site region using Protein Design Automation (PDA) as described in W098/47089. By visual inspection, the following residues were identified as belonging to the Core of Bacillus circulans **xylanase**: Y26, V28, W30, F36, V38, I51, Y53, A55, W58, G62, G64, L66, L68, G70, T72, I77, Y79, V81, Y105, I107, S130, A142, I144, F146, W153, M169, T171, G173, S176, G178, S180, V182, and V184. A rotamer group was assigned to each CORE position which allowed this position to become any phobic residue with the exception of methionine (i.e, Ala, Val, Leu, Ile, Phe, Tyr, and Trp) plus the original wild type residue. In the following PDA design only the CORE residues were allowed to **mutate** to any amino acid rotamer restricted by the definition of the rotamer group assigned to this position. The rest of the protein was treated as a template, with fixed coordinates. An energy cutoff of 50 kcal/mol for the rotamer/template energy was used to exclude unfavorable rotamers. The Van der Waals radius was scaled by a factor of 0.9 and the solvation model 2 as defined by Street and Mayo was used. The ground state rotamer sequence was extracted from all the possible rotamer sequences using the Dead End Elimination (DEE) method. To check for other low energy sequences a Monte Carlo (MC)

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search was performed starting from the DEE ground state. The PDA calculation resulted in a ground state sequence given in the specification. This sequence showed 13 **mutations** when compared to the wild type B.circulans **xylanase** sequence, Y26F, V28I, W30F, Y53F, W58F, G64V, Y79F, Y105F, A142L, T171L, S176A, S180A, and V182I. This state showed 93% identity with the complete wild type B.circulans **xylanase** sequence and had 60% identity in the designed positions with the wild type sequence. Using the Monte Carlo technique a list of low energy sequences was generated. Out of the lowest 1000 sequences generated by Monte Carlo none had more than 20 **mutations** from the wild type sequence and out of the lowest 101 sequences none had more than 18 **mutations**. Any protein sequence showing **mutations** at the above positions generated a more stable and/or active XA protein. (121 pages)

L4 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 1
 ACCESSION NUMBER: 2000:816350 CAPLUS
 DOCUMENT NUMBER: 135:14921
 TITLE: Molecular characterization of xynX, a gene encoding a multidomain **xylanase** with a thermostabilizing domain from Clostridium thermocellum
 AUTHOR(S): Kim, H.; Jung, K. H.; Pack, M. Y.
 CORPORATE SOURCE: Department of Agricultural Chemistry, Sunchon National University, Sunchon, 540-742, S. Korea
 SOURCE: Applied Microbiology and Biotechnology (2000), 54(4), 521-527
 CODEN: AMBIDG; ISSN: 0175-7598
 PUBLISHER: Springer-Verlag
 DOCUMENT TYPE: Journal
 LANGUAGE: English

AB A Clostridium thermocellum gene, xynX, coding for a **xylanase** was cloned and the complete nucleotide sequence was detd. The **xylanase** gene of Clostridium thermocellum consists of an ORF of 3261 nucleotide encoding a **xylanase** (XynX) of 1087 amino acid residues (116 kDa). Sequence anal. of XynX showed a multidomain structure that consisted of four different domains: an N-terminal thermostabilizing domain homologous to sequences found in several thermophilic enzymes, a catalytic domain homologous to family 10 glycosyl hydrolases, a duplicated cellulose-binding domain (CBD) homologous to family IX CBDs, and a triplicated S-layer homologous domain. A deletion **mutant** of xynX having only the catalytic region produced a **mutant** enzyme XynX-C which retained catalytic activity but lost thermostability. In terms of half-life at 70.degree.C, the thermostability of XynX-C was about six times lower than that of the other **mutant** enzyme, XynX-TC, produced by a **mutant** contg. both the thermostabilizing domain and the catalytic domain. The optimum temp. of XynX-C was about 5-10.degree.C lower than that of XynX-TC.
 REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 4 OF 6 Elsevier BIOBASE COPYRIGHT 2003 Elsevier Science B.V.
 ACCESSION NUMBER: 1996016919 ESBIOBASE
 TITLE: The conserved noncatalytic 40-residue sequence in cellulases and hemicellulases from anaerobic fungi functions as a protein docking domain
 AUTHOR: Fanutti C.; Ponyi T.; Black G.W.; Hazlewood G.P.; Gilbert H.J.
 CORPORATE SOURCE: H.J. Gilbert, Dept. of Biological/Nutritional Sci., University of Newcastle upon Tyne, Newcastle upon Tyne NE1 7RU, United Kingdom.
 SOURCE: Journal of Biological Chemistry, (1995), 270/49 (29314-29322)
 CODEN: JBCHA3 ISSN: 0021-9258
 DOCUMENT TYPE: Journal; Article

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COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Two cDNAs, designated xynA and manA, encoding **xylanase A (XYLA)** and mannanase A (MANA), respectively, were isolated from a cDNA library derived from mRNA extracted from the anaerobic fungus, *Piromyces*. XYLA and MANA displayed properties typical of endo-beta.1,4-**xylanases** and mannanases, respectively. Neither enzyme hydrolyzed cellulosic substrates. The nucleotide sequences of xynA and manA revealed open reading frames of 1875 and 1818 base pairs, respectively, coding for proteins of M(r) 68,049 (XYLA) and 68,055 (MANA). The deduced primary structure of MANA revealed a 458-amino acid sequence that exhibited identity with *Bacillus* and *Pseudomonas fluorescens* subsp. *cellulosa* mannanases belonging to glycosyl hydrolase Family 26. A 40-residue reiterated sequence, which was homologous to duplicated noncatalytic domains previously observed in *Neocallimastix patriciarum* **xylanase A** and endoglucanase B, was located at the C terminus of MANA. XYLA contained two regions that exhibited sequence identity with the catalytic domains of glycosyl hydrolase Family 11 **xylanases** and were separated by a duplicated 40-residue sequence that exhibited strong homology to the C terminus of MANA. Analysis of truncated derivatives of MANA confirmed that the N-terminal 458-residue sequence constituted the catalytic domain, while the C-terminal domain was not essential for the retention of catalytic activity. Similar deletion analysis of XYLA showed that the C-terminal catalytic domain homologue exhibited catalytic activity, but the corresponding putative N-terminal catalytic domain did not function as a **xylanase**. Fusion of the reiterated noncatalytic 40-residue sequence conserved in XYLA and MANA to glutathione S-transferase, generated a hybrid protein that did not associate with cellulose, but bound to 97- and 116-kDa polypeptides that are components of the multienzyme cellulase-hemicellulase complexes of *Piromyces* and *Neocallimastix patriciarum*, respectively. The role of this domain in the assembly of the enzyme complex is discussed.

L4 ANSWER 5 OF 6 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V.DUPLICATE

ACCESSION NUMBER: 1995:25116569 BIOTECHNO
TITLE: Evidence for a general role for non-catalytic thermostabilizing domains in **xylanases** from thermophilic bacteria
AUTHOR: Fontes C.M.G.A.; Hazlewood G.P.; Morag E.; Hall J.; Hirst B.H.; Gilbert H.J.
CORPORATE SOURCE: Dept Biological Nutritional Sciences, University of Newcastle upon Tyne, Newcastle upon Tyne NE1 7RU, United Kingdom.
SOURCE: Biochemical Journal, (1995), 307/1 (151-158)
CODEN: BIJOAK ISSN: 0264-6021
DOCUMENT TYPE: Journal; Article
COUNTRY: United Kingdom
LANGUAGE: English
SUMMARY LANGUAGE: English

AB A genomic library of *Clostridium thermocellum* DNA constructed in λ .ZAPII was screened for **xylanase**-expressing clones. Cross-hybridization experiments revealed a new **xylanase** gene isolated from the gene library, which was designated xynY. The encoded enzyme, **xylanase Y (XYLY)**, displayed features characteristic of an endo-beta.1,4-**xylanase**: the enzyme rapidly hydrolysed oat spelt, wheat and rye arabinoxylans and was active against methylumbelliferyl-beta.-D-cellobioside, but did not hydrolyse any cellulosic substrates. The pH and temperature optima of the enzyme were 6.8 and 75.degree.C respectively, and the recombinant XYLY, expressed by *Escherichia coli* had a maximum M(r) of 116 000. The nucleotide sequence of xynY contained an open reading frame of 3228 bp encoding a protein of predicted M(r) 120 105. The encoded enzyme contained a typical

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N-terminal 26-residue signal peptide, followed by a 164 amino acid sequence, designated domain A, that was not essential for catalytic activity. Downstream of domain A was a 351-residue **xylanase** Family F catalytic domain, followed by a 180-residue sequence that exhibited 28% sequence identity with a thermostable domain of *Thermoanaerobacterium saccharolyticum* **xylanase** A. The C-terminal portion of XYLY comprised the 23-residue duplicated docking sequence found in all other *C. thermocellum* plant cell wall hydrolases that are constituents of the bacterium's multienzyme complex, termed the cellulosome, followed by a 286-residue domain which exhibited 32% sequence identity with the N-terminal region of *C. thermocellum* **xylanase** Z. The enzyme did not contain linker sequences found in other *C. thermocellum* plant cell wall hydrolases. Analysis of truncated forms of XYLY and hybrid proteins, comprising segments of XYLY fused to the *E. coli* maltose binding domain, confirmed that XYLY contained a central catalytic domain and an adjacent thermostable domain. The C-terminal domain did not bind to cellulose or xylan. Western blot analysis using antiserum raised against XYLY showed that the **xylanase** was located in the cellulosome and did not appear to be extensively glycosylated. The non-catalytic domains of XYLY are discussed in relation to the general stability of thermophilic **xylanases**.

L4 ANSWER 6 OF 6 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1990:192771 CAPLUS

DOCUMENT NUMBER: 112:192771

TITLE: Nucleotide sequence and cloning in *Bacillus subtilis* of the *Bacillus stearothermophilus* pleiotropic regulatory gene *degT*

AUTHOR(S): Takagi, Masahiro; Takada, Hiroki; Imanaka, Tadayuki

CORPORATE SOURCE: Fac. Eng., Osaka Univ., Suita, 565, Japan

SOURCE: Journal of Bacteriology (1990), 172(1), 411-18

CODEN: JOBAAY; ISSN: 0021-9193

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The regulatory gene (*degT*) from *B. stearothermophilus* NCA1503 which enhanced prodn. of extracellular alk. protease (Apr) was cloned in *B. subtilis* with pTB53 as a vector. When *B. subtilis* MT-2 (Npr- [deficiency of neutral protease] Apr+) was transformed with the recombinant plasmid, pDT145, the plasmid carrier produced about three times more alk. protease than did the wild-type strain. In contrast, when *B. subtilis* DB104 (Npr- Apr-) was used as a host, the transformant with pDT145 could not exhibit any protease activity. After construction of the deletion plasmids, DNA sequencing was done. A large open reading frame was found, and nucleotide sequence anal. showed that the *degT* gene was composed of 1,116 bases (372 amino acid residues, mol. wt. of 41,244). A Shine-Dalgarno sequence was found 9 bases upstream from the open reading frame. A *B. subtilis* strain carrying *degT* showed the following pleiotropic phenomena: (i) enhancement of prodn. of extracellular enzymes such as alk. protease and levansucrase; (ii) repression of autolysin activity; (iii) decrease of transformation efficiency for *B. subtilis* (competent cell procedure); (iv) altered control of sporulation; (v) loss of flagella; and (vi) abnormal cell division. When *B. stearothermophilus* SIC1 was transformed with the recombinant plasmid carrying *degT*, the transformants exhibited abnormal cell division. These phenomena are similar to those of the phenotypes of *degSU*(Hy) (hyperprodn.), *degQ*(Hy), and *degR* mutants of *B. subtilis*. However, the amino acid sequence of the *degT* product (DegT) is different from those of the reported gene products. Furthermore, DegT includes a hydrophobic core region in the N-terminal portion (amino acid nos. 50-160), a consensus sequence for a DNA binding region (amino acid nos. 160-179), and a region homologous to transcription activator proteins (amino acid nos. 351-366). The membrane protein DegT may function as a sensor protein and transfer the signal of environmental stimuli to the regulatory region of target genes to activate or repress transcription of the genes.

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Hart, Edward

From: Rao, Manjunath N.
Sent: Tuesday, July 01, 2003 11:44 AM
To: Hart, Edward
Subject: Sequence search print out for 09/990,874

Hello Ed,

Below is the request regarding the application I mentioned in our phone conversation. In this case I am looking for variants and therefore I am not interested in 100% matches. Please rerun the search and provide me a print out of those results that have 3-10 or 3-15 mismatches in them. Please provide a print of at least 30-40 such results from each database. Thanks for all your help. If this is confusing to you please call me.

Thanks
Manjunath

From: Manjunath N. Rao
Art Unit 1652, Room 10A11
Mail Box in Room 10D 01
Phone: 306-5681

Date: 5-7-03

Please search the following as soon as possible for application with serial number **09/990874**

SEQ ID NO:16 against all commercial protein databases including issued patents database and pending application database and provide a print of all results.

If you have any questions please call me at the above phone number.

Thanks

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Manjunath N. Rao, Ph.D.
Biotechnology Patent Examiner
Art Unit 1652, Room 10A11
Mail Box in 10D01
Crystal Mall 1, USPTO.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2003, 11:47:38 ; Search time 27 Seconds
(without alignments)
207.050 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045

Sequence: 1 OTIQPCTGTCNMGCFYSYWND.....YQIVAVEGYFSSGSASITVS 190

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata1/1aa/5B_COMB.pep:*
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4: /cgn2_6/ptodata1/1aa/5B_COMB.pep:*
5: /cgn2_6/ptodata1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata1/1aa/backfilsl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1045	100.0	190	1	US-08-044-621D-26	Sequence 26, App1
2	1045	100.0	190	1	US-08-709-912-16	Sequence 16, App1
3	1045	100.0	190	2	US-09-047-370-16	Sequence 16, App1
4	1035	100.0	223	2	US-08-121-436A-2	Sequence 2, App1
5	1035	99.0	190	1	US-08-709-912-17	Sequence 17, App1
6	1035	99.0	190	2	US-09-047-370-17	Sequence 17, App1
7	1032	98.8	190	1	US-08-044-621D-27	Sequence 27, App1
8	1016	97.2	223	4	US-09-254-733-7	Sequence 7, App1
9	996	95.3	190	1	US-08-044-621D-28	Sequence 28, App1
10	996	95.3	190	1	US-08-709-912-14	Sequence 14, App1
11	996	95.3	190	2	US-09-047-370-14	Sequence 14, App1
12	721.9	69.1	261	4	US-08-768-373-2	Sequence 2, App1
13	665.9	63.7	225	1	US-08-290-979A-8	Sequence 8, App1
14	656.9	62.9	230	4	US-08-768-373-4	Sequence 2, App1
15	635.9	60.9	225	4	US-08-886-765-2	Sequence 4, App1
16	635.9	60.9	225	4	US-09-115-660-2	Sequence 2, App1
17	631.6	60.4	231	2	US-08-902-655A-6	Sequence 6, App1
18	631.6	60.4	231	2	US-08-507-431-6	Sequence 6, App1
19	631.6	60.4	236	3	US-09-116-622-6	Sequence 6, App1
20	631.6	60.4	236	4	US-09-219-277-6	Sequence 6, App1
21	620.9	59.4	226	4	US-09-599-661-6	Sequence 6, App1
22	620.9	59.4	227	1	US-08-458-023B-4	Sequence 4, App1
23	608.7	58.2	189	1	US-08-709-912-13	Sequence 13, App1
24	608.7	58.2	189	1	US-09-047-370-13	Sequence 13, App1
25	597.5	57.2	344	2	US-08-468-812-2	Sequence 2, App1
26	597.5	57.2	344	4	US-08-590-563-2	Sequence 2, App1
27	597.4	57.2	206	1	US-08-315-695-19	Sequence 19, App1

28	593.4	56.8	215	1	US-08-044-621D-34	Sequence 34, App1
29	591.4	56.6	191	1	US-08-709-912-10	Sequence 10, App1
30	591.4	56.6	191	2	US-09-047-370-10	Sequence 10, App1
31	568.3	54.4	197	1	US-08-044-621D-29	Sequence 29, App1
32	568.3	54.4	197	1	US-08-709-912-9	Sequence 9, App1
33	568.3	54.4	197	2	US-09-047-370-9	Sequence 9, App1
34	543.9	52.0	278	3	US-09-260-283-2	Sequence 2, App1
35	533.3	51.0	211	1	US-08-575-664-1	Sequence 1, App1
36	533.3	51.0	211	2	US-08-963-500-1	Sequence 1, App1
37	533.2	51.0	216	1	US-08-315-695-20	Sequence 20, App1
38	532.9	51.0	368	3	US-08-591-685-13	Sequence 13, App1
39	532.2	50.9	200	1	US-07-744-570B-2	Sequence 2, App1
40	531.5	50.9	189	1	US-08-044-621D-33	Sequence 33, App1
41	531	50.8	191	1	US-08-044-621D-35	Sequence 35, App1
42	529.5	50.7	189	1	US-08-709-912-12	Sequence 12, App1
43	529.5	50.7	189	2	US-09-047-370-12	Sequence 12, App1
44	529	50.6	191	1	US-08-709-912-11	Sequence 11, App1
45	529	50.6	191	2	US-09-047-370-11	Sequence 11, App1

ALIGNMENTS

RESULT 1
US-08-044-621D-26
; Sequence 26, Application US/08044621D
; Patent No. 5405769
; GENERAL INFORMATION:
; APPLICANT: Warren W. Makarchuk
; APPLICANT: Wing L. Sung
; APPLICANT: Makoto Yaeguchi
; APPLICANT: Robert L. Campbell
; APPLICANT: David R. Rose
; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gowling, Strathly & Henderson
; STREET: Suite 2600, 160 Elgin Street
; CITY: Ottawa
; STATE: Ontario
; COUNTRY: Canada
; ZIP: K1P 1C3
; MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,621D
; FILING DATE: April 8, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Judy A. Erratt
; REGISTRATION NUMBER: 34,076
; REFERENCE/DOCKET NUMBER: 08-863796
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 613-786-0199
; TELEFAX: 613-563-9869
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190
; TYPE: Amino Acid
; STRANDEDNESS: No
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: NO
; HYPOTHEICAL: NO
; ANTI-SENSE: NO

FRAGMENT TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Trichoderma reesei, XYN II, 21KD, PI 9.0
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Torronene, A., Mach, R.L., Messner, R.,
AUTHORS: Gonzalez, R., Kalkkinnen, N., Harkki, A.,
AUTHORS: Kubicek, C.P.
TITLE:
JOURNAL: Bio/Technology
VOLUME: 10
ISSUE:
PAGES: 1461-1465
DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-26

Query Match 100.0%; Score 1045; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 OTTQPGTGYNNNGYFYSYWMDHGGVYTTNGPGGQFYSVMSNSGNTFYVGGKMGQPTKTKKVI 60
QY 61 NFSGSYNPNNGNSLYSVGWSRNPLEYIYVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 120
DB 61 NFSGSYNPNNGNSLYSVGWSRNPLEYIYVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 120
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DB 121 ORVNOPSTIGTATFYQYWSVRRNRHSSGSVNTANHFMAAQGLTGTMDYQIIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 2
US-08-709-912-16
Sequence 16, Application US/08709912
Patent No. 5759840

GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039, 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO

FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Xyn II

PUBLICATION INFORMATION:
AUTHORS: Torronene, A
AUTHORS: Mach, R. L.
AUTHORS: Messner, R
AUTHORS: Gonzalez, R
AUTHORS: Kalkkinnen, N
AUTHORS: Harkki, A
AUTHORS: Kubicek, C. P.
JOURNAL: Biotechnology
VOLUME: 10
PAGES: 1461-1465
DATE: 1992
US-08-709-912-16

Query Match 100.0%; Score 1045; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTTQPGTGYNNNGYFYSYWMDHGGVYTTNGPGGQFYSVMSNSGNTFYVGGKMGQPTKTKKVI 60
DB 1 OTTQPGTGYNNNGYFYSYWMDHGGVYTTNGPGGQFYSVMSNSGNTFYVGGKMGQPTKTKKVI 60
QY 61 NFSGSYNPNNGNSLYSVGWSRNPLEYIYVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 120
DB 61 NFSGSYNPNNGNSLYSVGWSRNPLEYIYVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 120
QY 121 ORVNOPSTIGTATFYQYWSVRRNRHSSGSVNTANHFMAAQGLTGTMDYQIIVAVEGYF 180
DB 121 ORVNOPSTIGTATFYQYWSVRRNRHSSGSVNTANHFMAAQGLTGTMDYQIIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 3
US-09-047-370-16
Sequence 16, Application US/09047370
Patent No. 5866408

GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194


```

:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/047,370
: FILING DATE:
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 08/709,912
: FILING DATE: 09-SEP-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Olesen Mr. Warren E
: REGISTRATION NUMBER: 27290
: REFERENCE/DOCKET NUMBER: 1039.2000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 758-2400
: TELEFAX: (212) 758-2982
: INFORMATION FOR SEQ. ID NO.: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 190 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: internal
: ORIGINAL SOURCE:
: ORGANISM: Trichoderma reesei
: STRAIN: Xyn II
: PUBLICATION INFORMATION:
: AUTHORS: Tortorene, A
: AUTHORS: Mach, R. L.
: AUTHORS: Messner, R
: AUTHORS: Gonzalez, R
: AUTHORS: Kalkkinen, N
: AUTHORS: Harkki, A
: AUTHORS: Kubicek, C. P.
: JOURNAL: Biotechnology
: VOLUME: 10.
: PAGES: 1461-1465
: DATE: 1992
: US-09-047-370-16

Query Match          100.0%; Score 1045; DB 2: Length 190;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTIOPCTGNNNGFYFYSYWMNDHGCVYTYTNGPGGQFVSVMNSNGNFVGGKGMOPGTNNKYI 60
DB 1 QTIOPCTGNNNGFYFYSYWMNDHGCVYTYTNGPGGQFVSVMNSNGNFVGGKGMOPGTNNKYI 60
QY 61 NFGSYNPNNGNSLYSVYGMRSNPLLEYIIVENFGTYNPSTGATKLGVEVTSDSGVYDIYRT 120
DB 61 NFGSYNPNNGNSLYSVYGMRSNPLLEYIIVENFGTYNPSTGATKLGVEVTSDSGVYDIYRT 120
QY 121 QRYNOPSITIGTATFYQYWSVRRNRHSSGSVNTANHNANAAOGLTLGTMDYQIIVAVEGYF 180
DB 121 QRYNOPSITIGTATFYQYWSVRRNRHSSGSVNTANHNANAAOGLTLGTMDYQIIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 4
US-08-121-436A-2
: Sequence 2, Application US/08121436A
: Patent No. 5837515
: GENERAL INFORMATION:
: APPLICANT: Suominen, Pirkko
```

```

:
: APPLICANT: Nevalainen, Helena
: APPLICANT: Saarelainen, Ritva
: APPLICANT: Paloheimo, Marja
: APPLICANT: Lantinen, Tarja
: APPLICANT: Fagerstr m, Richard
: TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox
: STREET: 1100 New York Avenue, Suite 600
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/121,436A
: FILING DATE: 16-SEP-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/078,478
: FILING DATE: 18-JUN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/FI93/00221
: FILING DATE: 24-MAY-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/889,893
: FILING DATE: 29-MAY-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/524,308
: FILING DATE: 16-MAY-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Cimbala, Michele A.
: REGISTRATION NUMBER: 33,851
: REFERENCE/DOCKET NUMBER: 1050.008000C
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ. ID NO.: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 223 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-121-436A-2

Query Match          100.0%; Score 1045; DB 2: Length 223;
Best Local Similarity 100.0%; Pred. No. 3.3e-50;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTIOPCTGNNNGFYFYSYWMNDHGCVYTYTNGPGGQFVSVMNSNGNFVGGKGMOPGTNNKYI 60
DB 1 QTIOPCTGNNNGFYFYSYWMNDHGCVYTYTNGPGGQFVSVMNSNGNFVGGKGMOPGTNNKYI 60
QY 34 QTIOPCTGNNNGFYFYSYWMNDHGCVYTYTNGPGGQFVSVMNSNGNFVGGKGMOPGTNNKYI 93
DB 34 QTIOPCTGNNNGFYFYSYWMNDHGCVYTYTNGPGGQFVSVMNSNGNFVGGKGMOPGTNNKYI 93
QY 61 NFGSYNPNNGNSLYSVYGMRSNPLLEYIIVENFGTYNPSTGATKLGVEVTSDSGVYDIYRT 120
DB 61 NFGSYNPNNGNSLYSVYGMRSNPLLEYIIVENFGTYNPSTGATKLGVEVTSDSGVYDIYRT 120
QY 94 NFGSYNPNNGNSLYSVYGMRSNPLLEYIIVENFGTYNPSTGATKLGVEVTSDSGVYDIYRT 153
DB 94 NFGSYNPNNGNSLYSVYGMRSNPLLEYIIVENFGTYNPSTGATKLGVEVTSDSGVYDIYRT 153
QY 121 QRYNOPSITIGTATFYQYWSVRRNRHSSGSVNTANHNANAAOGLTLGTMDYQIIVAVEGYF 180
DB 121 QRYNOPSITIGTATFYQYWSVRRNRHSSGSVNTANHNANAAOGLTLGTMDYQIIVAVEGYF 180
QY 154 QRYNOPSITIGTATFYQYWSVRRNRHSSGSVNTANHNANAAOGLTLGTMDYQIIVAVEGYF 213
DB 154 QRYNOPSITIGTATFYQYWSVRRNRHSSGSVNTANHNANAAOGLTLGTMDYQIIVAVEGYF 213
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190
QY 214 SSGSASITVS 223
DB 214 SSGSASITVS 223

RESULT 5
US-08-709-912-17
```

Sequence 17, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L.
APPLICANT: Ishikawa Dr., Makoto
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Ujie, M
AUTHORS: Watson, D. C.
AUTHORS: Wakarchuk, W.
JOURNAL: Xylan and Xylanase
PAGES: 149-154
DATE: 1992
US-08-709-912-17

Query Match 99.0%; Score 1035; DB 1; Length 190;
Best Local Similarity 98.9%; Pred. No. 8.6e-50;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OTTQPGTGVNNGFYFYSYWDHGGVYTTNGPGGQFSVNMNSGNSGFVGKGMQPGTKNKVI 60
DB 1 OTTQPGTGVNNGFYFYSYWDHGGVYTTNGPGGQFSVNMNSGNSGFVGKGMQPGTKNKVI 60
QY 61 NFGSGYNPNNGNSLVSYGWRNPLIEYIYENGTNPSGTGAKRLGEVTSDSGVYDIYRT 120
DB 61 NFGSGYNPNNGNSLVSYGWRNPLIEYIYENGTNPSGTGAKRLGEVTSDSGVYDIYRT 120
QY 121 QRYNOPSIICTATFYQYWSYRRNHRSSGSVNTANHFNAMAQOGLTGTMDYQIYAVEGYF 180
DB 121 QRYNOPSIICTATFYQYWSYRRNHRSSGSVNTANHFNAMAQOGLTGTMDYQIYAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

Db 181 SSGSASITVS 190
RESULT 6
US-09-047-370-17
Sequence 17, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L.
APPLICANT: Yaguchi Dr., Makoto
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Ujie, M
AUTHORS: Watson, D. C.
AUTHORS: Wakarchuk, W.
JOURNAL: Xylan and Xylanase
PAGES: 149-154
DATE: 1992
US-09-047-370-17

Query Match 99.0%; Score 1035; DB 2; Length 190;
Best Local Similarity 98.9%; Pred. No. 8.6e-50;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OTTQPGTGVNNGFYFYSYWDHGGVYTTNGPGGQFSVNMNSGNSGFVGKGMQPGTKNKVI 60
DB 1 OTTQPGTGVNNGFYFYSYWDHGGVYTTNGPGGQFSVNMNSGNSGFVGKGMQPGTKNKVI 60

QY	6	NFGSGSNPNNGNSLSTVYGSNRPLLEYIVENEFYNPSGTATKLGEXTSGGSYDLYRT	120
Db	61	NFGSGSNPNNGNSLSTVYGSNRPLLEYIVENEFYINPSTGATKLGEXTSDGSYDLYRT	120
QY	121	QARNQPSIIIGTATFYQYMSVRPNRRHSSGSVNTANFNEMAAQOGLTGMDOYIAVEGYF	180
Db	121	QARNQPSIIIGTATFYQYMSVRPTRHSSGSVNTANFNEMAAQOGLTGMDOYIAVEGYF	180
QY	181	SSGSASITVS 190	
Db	181	SSGSASITVS 190	

RESULT 7
US-08-044-621D-27

Sequence 27, Application US/08044621D
Patent No. 5405769

GENERAL INFORMATION:

APPLICANT: Warren W. Wakarchuk
APPLICANT: Wing L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Gowling, Strathy & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360kB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Erratt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:

INFORMATION FOR SEQ. ID NO.: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 190
TYPE: Amino Acid
STRANDEDNESS: No. 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
STRAIN: Trichoderma viride, 20kD
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Yaguchi M., Roy C., Ujile M., Watson
AUTHORS: D.C., & Wakarchuk W.

```

1  TITLE:  Amino Acid Sequence of the low-Molecular-
2  TITLE:  Weight xylanase from Trichoderma viride
3  JOURNAL:  Xylans and Xylanases
4  VOLUME:
5  ISSUE:
6  PAGES:  149-154
7  DATE:   1992
8  DOCUMENT NUMBER:
9  FILING DATE:
10 PUBLICATION DATE:
11 RELEVANT RESIDUES IN SEQ ID NO:
12 US-08-044-621D-27

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Query Match	98.8%	Score 1032;	DB 1;	Length 190;
Best Local Similarity	98.48%	Pred. No. 1,3e-49;		
Matches 187; Conservative	2;	Mismatches 1;	Indels 0;	Gaps 0

[illegible]

RESULT 8
 US-09-254-733-7
 : Sequence 7: Application US/09254733
 : Patent No. 6277596
 : GENERAL INFORMATION:
 : APPLICANT: WATANABE, MANABU
 : APPLICANT: MORIYA, TATSUKI
 : APPLICANT: AOYAGI, KAORU
 : APPLICANT: SUMIDA, NAOMI
 : APPLICANT: MURAKAMI, TAKESHI
 : TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE CBHI GENES ORIGINATING
 : TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
 : TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH.
 : FILE REFERENCE: 99-0266*/LC(WMC)/00144
 : CURRENT APPLICATION NUMBER: US/09/254,733
 : NUMBER OF SEQ ID NOS: 52
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 7
 : LENGTH: 223
 : TYPE: PRT
 : ORGANISM: TRICHODERMA VIRIDE MC300-1
 : US-09-254-733-7

Query Match	97.2%	Score 1016:	DB 4	Length 223:
Best Local Similarity	96.8%:	Pred. No. 1.3e+48:		
Matches 184:	Conservative 2:	Mismatches 4:	Indels 0:	Gaps 0
QY	1	QTIOPTCTYNNNGYFYSYVNDNDCGCVTYNNGPCGQFESVMMNSGNGFVGGKGMQPTGKKNKYI	60	
Db	34	QTIQPTGTNNNGYFYSYVNDNDCGCVTYNNGPCGQFESVMMNSGNGFVGGKGMQPTGKKNKYI	93	
QY	61	NFSGSYNPNNGSYLSVYGVMSRNPLEYIIVENFGTYNPSTGATKLGCVTSDCSVYDIYRT	120	
Db	94	NFSGTYNPNNGSYLSVYGVMSRNPLEYIIVENFGTYNPSTGATKLGCVTSDCSVYDIYRT	153	
QY	121	QRVNPDSLTIGATFQYVMSVRNRHNSGSVNTANFNFMMAOQGLLTGMDDVQIVAVEGFF	180	
Db	154	QRVNPDSLTIGATFQYVMSVRNRHNSGSVNTANFNFMMAASHGLLTGMDDVQIVAVEGFF	213	

OY 181 SSGSASTVS 190
Db 214 SSGSASTVS 223

RESULT 9

US-08-044-621D-28
Sequence 28, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Makarchuk
APPLICANT: Wing L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gowling, Strathy & Henderson
STREET: Suite 2600, 160 Elgin Street
City: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Erralt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 190
TYPE: Amino Acid
STRANDEDNESS: NO, 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Trichoderma harzianum
STRAIN: Trichoderma harzianum, 20kd
IMMEDIATE SOURCE:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin
AUTHORS: F., Tan L.U.L., Senior D.J., & Saddler
AUTHORS: J.N.
TITLE:
JOURNAL: Xylans and Xylanases
VOLUME:
ISSUE:
PAGES: 435-438
DATE: 1992

DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-28

Query Match 95.3%; Score 996; DB 1; Length 190;
Best Local Similarity 94.7%; Pred. No. 1,2e-47;
Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 QTIQPGTGNNGYFYSWANDHGGVYTYNGPGQFVSVMNSNGNFVGKGMQPGTKNKVI 60
Db 1 QTIQPGTGNNGYFYSWANDHGGVYTYNGPGQFVSVMNSNGNFVGKGMQPGTKNKVI 60
OY 61 NFGSYNPNGNSLSYVWGRNPLIEYIYENFTYNTSPGARKLEGVTSDSGVYDIYRT 120
Db 61 NFGSYNPNGNSLSYVWGRNPLIEYIYENFTYNTSPGARKLEGVTSDSGVYDIYRT 120
OY 121 QRVNPSIICTATFYQWVSRNRHSSGSVNTANHFNAMAQGLTGTMDYQIVAVEGYE 180
Db 121 QRVNPSIICTATFYQWVSRNRHSSGSVNTANHFNAMAQGLTGTMDYQIVAVEGYE 180
OY 181 SSGSASTVS 190
Db 181 SSGSASTVS 190

RESULT 10

US-08-709-912-14
Sequence 14, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Ming L.
APPLICANT: Yaguchi Dr., Makoto
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Filzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
City: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039,2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:


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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0540003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO.: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
FEATURE:
NAME/KEY: Protein
LOCATION: 1..230
OTHER INFORMATION: /label= XLNB
US-08-768-373-4

```

```

Query Match          62.9%   Score 656.9; DB 4; Length 230;
Best Local Similarity 64.1%; Pred. No.7.5e-29;
Matches 118; Conservative 23; Mismatches 42; Indels 1; Gaps 1

QY      6 GTGYNNGCYFYYSWMDHGCVTTNPGCGOFSVNMNSNGNFVGCKGMOPOTKKNVINFGSS 65
       111 ::::111: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      45 GTGTHTNGMYISFMFTDGGGTVMVTYTNNGGSYSVNMCNCNCFVCGKKMRIGAA-ATIKYSN 103
       ||| :|||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      66 YNPNGNSTLASYGMSRNPLIEIYEENGTINPSTGATKLGESVSDGSYYDIYFQRVNO 125
       ||| :|||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      104 YNPGNSTLAIYGWRNPLVEYIIVESGYTDPSGAONLTGFOSDGDTGYIAKSTRYNA 163
       ||| :|||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      126 PSITGATFFYOWSVRRNRHSSGSVNTANHFAMAOOGILTGMTYOIVAVEGYSSGSA 185
       ||| :|||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      164 PSTECTKTFTYWSVRTSKRVGVGTVANHFEMAKSKGLNLSHDYQIVATEGYRSSGSA 223
       ||| :|||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      186 SITV 189
       |||
DB      224 SITV 227

RESULT 15
US-08-886-765-2
: Sequence 2, Application US/08886765
: Patent No. 5817500
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
APPLICANT: Wagner, Peter
APPLICANT: Mullertz, Anette
APPLICANT: Knapp, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSSEE: No. 5817500 No. 5817500disk of No. 5817500th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-886-765-2

Query Match      60.9%; Score 635.9; DB 2; Length 225;
Best Local Similarity 60.2%; Pred. No. 1e-27;
Matches 115; Conservative 28; Mismatches 47; Indels 1; Gaps 1;

Oy   1 OTIQPCRYNNGYRYSVYNDDHGCVTYNPGCGQPSVWMSNSGNPVGSKGMOPGKKNVI 60
    || :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   32 QTTPNSEBWHGGYYISWSDDGAQTATYNLBGTYEISWGOGNLTVGKGMPGLNAHAI 91
Oy   61 NFGSYNENGNSIYSVYGMSRNPLIEYIVENFGYNPSTGATKIGEVTSDGSVDIYRT 120
Db   92 HFEVGYQNGNSYLAVYGMTNRPLEV EYIVENFGTYPDSSCATDLCTYECCOS IYRLCKT 151
Oy   121 QRVNOSTITATYTYQYWSVRNRHRSSGSVNTANHFNMAAOGLTL-CTMDIYVAVECY 179
    ||| |||| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   152 TRVNAVSDIGQTFPDQYWSVRQDRKTSQTVOTGCHFDAMARAGLNVNDHYIVATPKY 211
Oy   180 FSSGSASTVS 190
    |||| | |||:
Db   212 FSSGYARTVA 222

RESULT 16
US-09-115-660-2
Sequence 2, Application US/09115660
Patent No. 6245546
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
APPLICANT: Wagner, Peter
APPLICANT: Mullertz, Anette
APPLICANT: Knapp, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: No. 62455460 No. 6245546disk of No. 6245546th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,660
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

```



```

? NAME: Harrington, James J.
? REGISTRATION NUMBER: 38,711
? REFERENCE/DOCKET NUMBER: 3954.204-US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 212-867-0123
? TELEFAX: 212-878-9655
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 296 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-507-431-6

```

Query Match	60.4%	Score 631.6	DB 1	Length 296
Best Local Similarity	61.5%	Pred. No. 3e-27		
Matches 115	Conservative 26	Mismatches 42	Indels 4	Gaps 3

QY 7 TGTANNQYFPFSYAMDG - HGCVTYTNPGCGFYSYVMSNSCNPFYGGKMKQCGTKNKVYNISGS 65
 Db 46 TGTSMNYYYSPMTDGAASGDVEYSNCAAGGSYSYTWSSASNPFYGGKMKMNNGSAHD - IYTSGS 104
 QY 66 YND - NGNSYLSVYGGKSRNPDI EYIVENFGTYNPGTATKLG EYTSDGSGVYDIYRTQRY 123
 Db 105 WTSTGNSNSYLSVYGGTGTPLVEYIYLEDYGEYNSGASGYTKGSAVSDQSYTYNIYATRT 164
 QY 124 NQSIITGATFFQYVSWRRNRHSSGSVYNTANFNFMMAAQGLTGMDYQIYAVEGYSFGS 183
 Db 165 NMSISDGTATFQOYMSIRQTKRVGGTYTTANFNFMMAALGNNLGHNTQIYATEGEGYSSG 224
 QY 184 SASITVS 190
 Db 225 SASITVA 231

RESULT 19
US-09-116-622-6
Sequence 6, Application US/09116622
Patent No. 6080567
GENERAL INFORMATION:
APPLICANT: Kotofod, Lene V.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Christgau, Stephan
APPLICANT: Heldt-Hansen, Hans P.
APPLICANT: Dalboge, Henrik
APPLICANT: Andersen, Lene N.
APPLICANT: Si, Joan O.
APPLICANT: Jacobson, Tina
APPLICANT: Munk, Niels
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
TITLE OF INVENTION: ASPERGILLUS ACULEATUS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 60805670 No. 6080567disk of No. 6080567th America, Inc
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116.622
FILING DATE: 16-July-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Agtis, Cheryl H.
REGISTRATION NUMBER: 34, 086
REFERENCE/DOCKET NUMBER: 3954.224-US

```

? TELECOMMUNICATION INFORMATION
? TELEPHONE: 212-867-0123
?
? TELEFAX: 212-878-9655
?
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 296 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
? NS-09-116-622-6

```

Query Match	60.4%	Score	631.6	DB	3	Length	256
Best Local	Similarity	61.5%	Pred	No.	3e-27		
Matches	115	Conservative	26	Mismatches	42	Indels	4
						Gaps	3

QY 7 TGVNNGVFPFYSYMDG - HGVVYTNNGPGGGEFYSVMSNSGNPFVGGKGMOPGTSTNKIYNISGS 65
Db 46 TGVSNCTYYTSFMTDGCASGDVEYSNAGSGYSVTWSSASNPVGGCKGMNNGASHD - ITTSGS 104
QY 66 YNP - NGNSYLSVYGMNSRNPALLEYIVENFGTYNPSTGATKLEGYSDGSGVYDIYTRQRY 123
Db 105 WTSTGNSNSLSVYGGWTTGPLVEYIYLEDGYENPGSAGTYKGSVSDSGSYNYINITYATRT 164
QY 124 NQSTIICTATFPQYVMSVRNRHSSGSVNTAHNFNMAAQGLTLGTMDOYIAYVCGYFSSG 183
Db 165 NMSISDGTATFPQYMSIRQTKRFGCGVTYTAHNFNMAALGNLGHNYQIYATGEGYSSG 224
QY 184 SASITVS 190
Db 225 SASITVA 231

RESULT 20
US-09-219-277-6
: Sequence 619 Application US/09219277
Patent No. 6197564
: GENERAL INFORMATION:
: APPLICANT: Kofod, Lene V.
: APPLICANT: Kauppinen, Markus S.
: APPLICANT: Christgau, Stephan
: APPLICANT: Heidt-Hansen, Hans P.
: APPLICANT: Dalboge, Henrik
: APPLICANT: Andersen, Lene N.
: APPLICANT: Si, Joan O.
: APPLICANT: Jacobson, Tina
: APPLICANT: Munk, Niels
: APPLICANT: Mullertz, Anette
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
TITLE OF INVENTION: ASPERGILLUS ACULEATUS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61975640 No. 6197564disk Of No. 6197564th America, Inc
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/219,277
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/116,622
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Agtis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3954.224-US

REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 215
TYPE: Amino Acid
STRANDEDNESS: No, 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No
ORIGINAL SOURCE:
ORGANISM: Streptomyces lividans
STRAIN: Streptomyces lividans, xln B
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Shareck, F., Roy, C., Yaguchi, M.,
AUTHORS: Morosoli, R. & Kluepfel, D.
TITLE:
JOURNAL: Gene
VOLUME: 107
ISSUE:
PAGES: 75-82
DATE: 1991
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-34

Query Match 56.8%; Score 593.4; DB 1; Length 215;
Best Local Similarity 57.1%; Pred. No. 2.1e-25;
Matches 108; Conservative 33; Mismatches 42; Indels 6; Gaps 5;

QY 2 TTTPGCGYNNNGYFYSWNDGCGVYTYTNGCGOFSYVNMNSGNGFVGGKGMOPCTKKKYN 61
DB 6 TNEGCT--NNGYYSFTWDSQGTYSNMKSGGQYSTSMRTGTFVAGKGMANGR-RTYO 62
QY 62 FSGSYNPNNGSYLVSYVSGSRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRTQ 121
DB 63 YSGSFNPSGNAYLALYGWTSNPLVEYIYVDMNGTYRP-TGEYK-GVYTSDCGTYDIYKTT 120
QY 122 RVNOPSIICTATFYQYVSVRRNHRSSGSVNTANHFANAAOQGLTGTMD-YQIVAVEGYF 180
DB 121 RVNKPVEEGTRTFDQYVSVRQSKRTGTTTGNHFDAMARACMPLGNFSYIMINTEGYQ 180
QY 181 SSGSASTIV 189
DB 181 SSGTSSINV 189

RESULT 29
US-08-709-912-10
Sequence 10, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr., Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Streptomyces lividans
STRAIN: xln B
PUBLICATION INFORMATION:
AUTHORS: Shareck, F
AUTHORS: Roy, C
AUTHORS: Yaguchi, M
AUTHORS: Morosoli, R
AUTHORS: Kluepfel, D
JOURNAL: Gene
VOLUME: 107
PAGES: 75-82
DATE: 1991
US-08-709-912-10

Query Match 56.6%; Score 591.4; DB 1; Length 191;
Best Local Similarity 56.6%; Pred. No. 2.1e-25;
Matches 107; Conservative 34; Mismatches 42; Indels 6; Gaps 5;

QY 2 TTTPGCGYNNNGYFYSWNDGCGVYTYTNGCGOFSYVNMNSGNGFVGGKGMOPCTKKKYN 61
DB 6 TNEGCT--NNGYYSFTWDSQGTYSNMKSGGQYSTSMRTGTFVAGKGMANGR-RTYO 62
QY 62 FSGSYNPNNGSYLVSYVSGSRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRTQ 121
DB 63 YSGSFNPSGNAYLALYGWTSNPLVEYIYVDMNGTYRP-TGEYK-GVYTSDCGTYDIYKTT 120
QY 122 RVNOPSIICTATFYQYVSVRRNHRSSGSVNTANHFANAAOQGLTGTMD-YQIVAVEGYF 180
DB 121 RVNKPVEEGTRTFDQYVSVRQSKRTGTTTGNHFDAMARACMPLGNFSYIMINTEGYQ 180
QY 181 SSGSASTIV 189
DB 181 SSGTSSINV 189

RESULT 30
US-09-047-370-10
Sequence 10, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto

RELEVANT RESIDUES IN SEQ ID NO: 1;
US-08-044-621D-29

Query Match	54.48;	Score 568.3;	DB 1;	Length 197;
Best Local Similarity	55.08;	Pred. No. 4.2e-24;		
Matches 105;	Conservative 34;	Mismatches 45;	Indels 7;	Gaps 3

QY 7 TGTNNQYFPYSNNWDGCGCTTNGGCGGQFQVMS--NSQNFEGGKGMQPGTKNKIKNFSGS 65
Db 7 TGTDDGYYTSSWMTDAGDATTYNNNGGCTYLTWSSGNNNLVGGKGNRPGAASRSISYSGT 66
QY 66 YDNGNSYLSVYGWMSNPLEYIYVENFGTYNPSTGAKLGEVTSDGSVYDIYFTORVNO 125
Db 67 YQNGNSYLSVYGWTRKSLIEYIYVESYGSVDPSAASHKSGSYCNGATYDILSTWRYNA 126
QY 126 PSTLTGATGYQYWSVARNHRK-----SGSVNTAHNFENMAAOGLTLGT-NDYQIQAVEGY 179
Db 127 PSTIDGQTOTFEQFWSVNRPKAKGSGISGTVDOCFHFDAMKGLGNLSSEHYQIATEGY 186
QY 180 FSSGSASITVS 190
Db 187 QSSGTAITVT 197

RESULT 32
 US-08-709-912-9
 Sequence 9, Application US/08709912
 Patent No. 5739840
 GENERAL INFORMATION:
 APPLICANT: Sung Dr., Ming L
 APPLICANT: Yaguchi Dr., Makoto
 APPLICANT: Ishikawa Dr., Kazuhiko
 TITLE OF INVENTION: Modification of xylanase to improve
 TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
 STREET: 217 Park Ave.
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10172-0194
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/709,912
 FILING DATE: 09-SEP-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Olsen Mr, Warren E
 REGISTRATION NUMBER: 27290
 REFERENCE/DOCKET NUMBER: 1039, 2000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-2400
 TELEFAX: (212) 758-2982
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 197 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: Internal
 ORIGINAL SOURCE:
 ORGANISM: Schizosaccharomyces pombe
 STRAIN: Xylanase A
 PUBLICATION INFORMATION:

: AUTHORS: Oku, T
 : AUTHORS: Yaguchi, M
 : AUTHORS: Parse, M
 : AUTHORS: Jurasek, L
 : JOURNAL: Canadian Fed. Biol. Soc. annual meeting
 : PAGES: Abstract #676
 : DATE: 1988
 : US-08-709-912-9.

Query Match	54.48;	Score 568.3;	DB 1;	Length 197;
Best Local Similarity	55.08;	Pred. No. 4.2e-24;		
Matches 105;	Conservative 34;	Mismatches 45;	Indels 7;	Gaps

[illegible]

RESULT 33
US-09-047-370-9
Sequence 9, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
THERMOSTABILITY, Alkalophilicity and
THERMOSTABILITY
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047.370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039, 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO.: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
STRANDEDNESS: single.


```

? TOPOLOGY: linear
? MOLECULE TYPE: protein
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE: Internal
? ORIGINAL SOURCE:
? ORGANISM: Schizosaccharomyces pombe
? STRAIN: xylanase A
? PUBLICATION INFORMATION:
? AUTHORS: Oku, T
? AUTHORS: Taguchi, M
? AUTHORS: Parise, M
? AUTHORS: Jurasek, L
? JOURNAL: Canadian Fed. Biol. Soc. annual meeting
? PAGES: Abstract #676
? DATE: 1988
? US-09-047-370-9

Query Match
Best local Similarity 54.4%; Score 568.3; DB 2; Length 197;
Matches 105; Conservative 34; Mismatches 45; Indels 7; Gaps 3;

? 7 TGYNNGYFYVWNGHGVYTYNGPGQFVSVMNS-NSGNFVGKGMQPGTKKKNVINFSS 65
? ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
? 7 TGTDCGYYSMTDGDATYONNGGXYTLTWSGNMNLVGKGMNPGASRSISYSGT 66
? QY 66 YPNNGNSYLVYVWNGHGVYTYNGPGQFVSVMNS-NSGNFVGKGMQPGTKKKNVINFSS 125
? ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
? DB 67 YPNNGNSYLVYVWNGHGVYTYNGPGQFVSVMNS-NSGNFVGKGMQPGTKKKNVINFSS 126
? QY 126 YPNNGNSYLVYVWNGHGVYTYNGPGQFVSVMNS-NSGNFVGKGMQPGTKKKNVINFSS 179
? ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
? DB 127 YPNNGNSYLVYVWNGHGVYTYNGPGQFVSVMNS-NSGNFVGKGMQPGTKKKNVINFSS 186
? QY 180 FSSGSASIVS 190
? ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
? DB 187 OSSGATATVTF 197

RESULT 34
US-09-260-283-2
? Sequence 2, Application US/09260283
? Patent No. 6083734
? GENERAL INFORMATION:
? APPLICANT: CHUANG, Ming-Hon
? APPLICANT: JENG, King-Song
? APPLICANT: WU, Shaw-Yun
? APPLICANT: LIN, Lung-Shen
? APPLICANT: CHANG, Edward
? TITLE OF INVENTION: NOVEL RECOMBINANT XYLANASE, THE PREPARATION AND USE OF
? FILE REFERENCE: Chuang, et al
? CURRENT APPLICATION NUMBER: US/09/260,283
? CURRENT FILING DATE: 1999-03-02
? EARLIER APPLICATION NUMBER: 87103297
? EARLIER FILING DATE: 1998-03-06
? NUMBER OF SEQ ID NOS: 8
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 2
? LENGTH: 278
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Amino acid
? OTHER INFORMATION: sequence encoded by the recombinant xylanase gene
? OTHER INFORMATION: xylid 1
US-09-260-283-2

Query Match
Best local Similarity 52.0%; Score 543.9; DB 3; Length 278;
Matches 102; Conservative 39; Mismatches 48; Indels 11; Gaps 6;

? 1 QTIOP-GTGYNNGYFYVWNGHGVYTYNGPGQFVSVMNS-NSGNFVGKGMQPGTKKKNV 58
```

```

? ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
? 4 QTLSSNSTGTNGNPFYTFWKDS-GDASMTLSSGGRYQSSMGSTNNWVGKGMNPNNSR 62
? QY 59 YNFGSGY--NPNNGNSYLVYVWNGHGVYTYNGPGQFVSVMNS-NSGNFVGKGMQPGTKKKNV 114
? ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
? DB 63 VISYSGSYGVDSQNSYALYGVWTRSPLEIYVIESYSGYNPASCSCGTDGSPQSDAT 122
? QY 115 YDIYRORVNOPSTIGTAFYVWNGHGVYTYNGPGQFVSVMNS-NSGNFVGKGMQPGTKKKNV 170
? ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
? DB 123 YVNRQORVNOPSTIGTAFYVWNGHGVYTYNGPGQFVSVMNS-NSGNFVGKGMQPGTKKKNV 182
? QY 171 YQIVAVEGYFSSGSASIVS 190
? ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
? DB 183 YQIVAVEGYFSSGSASIVS 202

RESULT 35
US-08-575-964-1
? Sequence 1, Application US/08575964
? Patent No. 5736384
? GENERAL INFORMATION:
? APPLICANT: Fukunaga, No. 5736384yuk1
? APPLICANT: Iwasaki, Yui1
? APPLICANT: Kono, Satoko
? APPLICANT: Kita, Yukio
? APPLICANT: Izumi, Yoshiya
? TITLE OF INVENTION: THERMOSTABLE XYLANASE
? NUMBER OF SEQUENCES: 3
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Fish & Richardson P.C.
? STREET: 4225 Executive Square, Suite 1400
? CITY: La Jolla
? STATE: CA 92037
? COUNTRY: USA
? ZIP: 92037
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/575,964
? FILING DATE: 20-DEC-1995
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Haile, Lisa A.
? REGISTRATION NUMBER: 38,347
? REFERENCE/DOCKET NUMBER: 07898/002001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 619/678-5070
? TELEFAX: 619/678-5099
? TELEX: 200154
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 211 amino acids
? TYPE: amino acid
? STRANDEDNESS: not relevant
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? ORIGINAL SOURCE:
? ORGANISM: Bacillus sp.
? STRAIN: 2113
? FEATURE:
? OTHER INFORMATION: 1-23 S sig peptide.
? OTHER INFORMATION: 24-211 S mat peptide.
US-08-575-964-1

Query Match
Best local Similarity 51.0%; Score 533.3; DB 1; Length 211;
Matches 101; Conservative 28; Mismatches 45; Indels 7; Gaps 5;

? 14 FYVWNGHGVYTYNGPGQFVSVMNS-NSGNFVGKGMQPGTKKKNVINF-SGSYNPNNS 72
? ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
? ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```

Db 32 YMOYMTDGGGTATNATNGSGNYSVTWMSVGNFVVGKMGKGTGSPTRTVYNAGVWAPSNGC 91
OY 73 YLSVYGSRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVYDIYRTORVNOPSLIGTA 132
Db 92 YLTLYGWTNRSLIEYIVVDSMGTYRP-TGYRK-GTVSDGCTDIYITTMRYNAPSIDGTQ 149
OY 133 TFPQYMSVRNRHSSG---SVNTANHFNMAAOGGLTG-TMDYOIVAVEGYFSSGSASIT 188
Db 150 TFPQYMSVRQSKRPTGSNVSITFNSHNVMNRNMGMLGSSMAVOYLAVEGYQSSGSANVT 209
OY 189 V 189
Db 210 V 210

RESULT 36

US-08-963-500-1
Sequence 1, Application US/08963500

Patent No. 5916795
GENERAL INFORMATION:
APPLICANT: Fukunaga, No. 5916795uyuki
APPLICANT: Iwasaki, Yoji
APPLICANT: Kono, Satoko
APPLICANT: Kita, Yukio
APPLICANT: Izumi, Yoshiya
TITLE OF INVENTION: THERMOSTABLE XYLANASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: MA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,500
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/575,964
FILING DATE: 20-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07898/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacillus sp.
STRAIN: 2113
FEATURE:
OTHER INFORMATION: 1-23 S sig peptide.
US-08-963-500-1

Query Match 51.0% Score 533.3; DB 2; Length 211;
Best Local Similarity 55.8%; Pred. No. 4e-22;
Matches 101; Conservative 20; Mismatches 45; Indels 7; Gaps 5;

OY 14 FYSYNDHGCVTYTNGPCGQFSVMSNSGNFVGKMGWDPYTKNKYIN-FSGSYNPNGNS 72
Db 32 YMOYMTDGGGTATNATNGSGNYSVTWMSVGNFVVGKMGKGTGSPTRTVYNAGVWAPSNGC 91
OY 73 YLSVYGSRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVYDIYRTORVNOPSLIGTA 132
Db 92 YLTLYGWTNRSLIEYIVVDSMGTYRP-TGYRK-GTVSDGCTDIYITTMRYNAPSIDGTQ 149
OY 133 TFPQYMSVRNRHSSG---SVNTANHFNMAAOGGLTG-TMDYOIVAVEGYFSSGSASIT 188
Db 150 TFPQYMSVRQSKRPTGSNVSITFNSHNVMNRNMGMLGSSMAVOYLAVEGYQSSGSANVT 209
OY 189 V 189
Db 210 V 210

RESULT 37

US-08-315-695-20
Sequence 20, Application US/08315695

Patent No. 5591619
GENERAL INFORMATION:
APPLICANT: Li, Xin-Liang
APPLICANT: Ljungdahl, Lars G.
TITLE OF INVENTION: Aureobasidium pullulans xylanase, Gene
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,695
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P.
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 55-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 216 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-315-695-20

Query Match 51.0% Score 533.2; DB 1; Length 216;
Best Local Similarity 50.5%; Pred. No. 4.2e-22;
Matches 101; Conservative 31; Mismatches 50; Indels 18; Gaps 6;

OY 5 PGTY-----NGYFYSYNDHGCVTYTNGPGQFSVMSNSGNFVGKMGWOP 53
Db 21 PGTAHAATTITTTGOTGDMYYSFMTDGGGSVMTLNGGGSYSTQMTNCGNFVAGKGMST 80
OY 54 GTNKNKYNISGNSPNPNSLSLVYGSRNPLIEYIVENFGTYNPSTGATKLGCVTSDGS 113
Db 81 GDCN--VRVNGYENPVNGYGLYGMTSNPLVEYIVDMNGSYRP-TGYRK-GTVSSDGG 136

QY 114 VDIYRTORVNOPSLIGTATFYQWYSVRNRHSSGS--VNTANHFNMAOQGLTGTMD- 170
114 VDIYRTORVNOPSLIGTATFYQWYSVRNRHSSGS--VNTANHFNMAOQGLTGTMD- 170
Db 137 TYDIYETTRYNAPSEVGRKTFQOYWSVRSKVTSSGSLTTTGNHFDANARAGMNNQGFY 196
137 TYDIYETTRYNAPSEVGRKTFQOYWSVRSKVTSSGSLTTTGNHFDANARAGMNNQGFY 196
QY 171 YQIYAVEGYFSSGSASITVS 190
171 YQIYAVEGYFSSGSASITVS 190
Db 197 YIMATEGYSSGSSSNTIVS 216
197 YIMATEGYSSGSSSNTIVS 216

RESULT 38
US-08-591-685-13
Sequence 13, Application US/08591685
Patent No. 6083733
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Thermostable xylanases
NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,685
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-685-13

Query Match 51.0%; Score 532.9; DB 3; Length 368;
Best Local Similarity 57.1%; Pred. No. 1.2e-21;
Matches 108; Conservative 22; Mismatches 48; Indels 11; Gaps 6;

QY 7 TGYNNGYFYSYNNDCHGVTYTNPGGQPSVWMSNSGN--FYGGR----GW-QPGTKNRY 59
7 TGYNNGYFYSYNNDCHGVTYTNPGGQPSVWMSNSGN--FYGGR----GW-QPGTKNRY 59
Db 29 TGTYYGYEIMKD-TGNTTMTVDVGGRRSCQMSNNALFRTGKFFSTAMNQLGTVK-- 85
29 TGTYYGYEIMKD-TGNTTMTVDVGGRRSCQMSNNALFRTGKFFSTAMNQLGTVK-- 85

QY 60 INFSGSYNPNNGNSYLSVYGSNRNPLIEYIYVENFGYNSGTATKIGEYTSQSYDIYR 119
60 INFSGSYNPNNGNSYLSVYGSNRNPLIEYIYVENFGYNSGTATKIGEYTSQSYDIYR 119
Db 86 IITYSATYNPNGNSYLCITGMSRNPLEYEVIVSWGSMRP-PEATSLIGTYTIDGATYDIYK 144
86 IITYSATYNPNGNSYLCITGMSRNPLEYEVIVSWGSMRP-PEATSLIGTYTIDGATYDIYK 144

QY 120 TORVNOPSLIGTATFYQWYSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIYAVEGY 179
120 TORVNOPSLIGTATFYQWYSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIYAVEGY 179
Db 145 TTRVNOPSLIGTATFYQWYSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIYAVEGY 204
145 TTRVNOPSLIGTATFYQWYSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIYAVEGY 204

QY 180 FSSGSASIT 188
180 FSSGSASIT 188
Db 205 OSSGSANIT 213
205 OSSGSANIT 213

RESULT 39
US-07-744-570B-2
Sequence 2, Application US/07744570B
Patent No. 5202249
GENERAL INFORMATION:
APPLICANT: Kluempfel, D.
APPLICANT: Morosoli, R.
APPLICANT: Shareck, F.
TITLE OF INVENTION: Xylanase for Biobleaching
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael J. Bradley
STREET: 1200 South 47th Street
STREET: Box Number 4023
CITY: Richmond
STATE: California
COUNTRY: United States

ZIP: 94804-0023
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44mb storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/744,570B
FILING DATE: 19910813
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: AMINO ACID
STRANDEDNESS: Single strand
TOPOLOGY: Circular
US-07-744-570B-2

Query Match 50.9%; Score 532.2; DB 1; Length 200;
Best Local Similarity 50.5%; Pred. No. 4.1e-22;
Matches 101; Conservative 30; Mismatches 51; Indels 18; Gaps 6;

QY 5 PGTY-----NNGEYFSYNNNDCHGVTYTNPGGQPSVWMSNSGNFYGGRKQWP 53
5 PGTY-----NNGEYFSYNNNDCHGVTYTNPGGQPSVWMSNSGNFYGGRKQWP 53
Db 4 PGTAAHATTITNTGTGDMYYSFWTDGGGSVSMTLNNGGYSYQTWNTGNGNFVACKWST 63
4 PGTAAHATTITNTGTGDMYYSFWTDGGGSVSMTLNNGGYSYQTWNTGNGNFVACKWST 63

QY 54 GTRKNVINFSGSYNPNNGNSYLSVYGSNRNPLIEYIYVENFGYNSGTATKIGEYTSQGS 113
54 GTRKNVINFSGSYNPNNGNSYLSVYGSNRNPLIEYIYVENFGYNSGTATKIGEYTSQGS 113
Db 64 GDCN--VRNNGYFNPVNGYGLVGTWSPNPLIEYIVDWMGSYRP-TGYRK-GTVSSDGG 119
64 GDCN--VRNNGYFNPVNGYGLVGTWSPNPLIEYIVDWMGSYRP-TGYRK-GTVSSDGG 119

QY 114 VDIYRTORVNOPSLIGTATFYQWYSVRNRHSSGS--VNTANHFNMAOQGLTGTMD- 170
114 VDIYRTORVNOPSLIGTATFYQWYSVRNRHSSGS--VNTANHFNMAOQGLTGTMD- 170
Db 120 TYDIYETTRYNAPSEVGRKTFQOYWSVRSKVTSSGSLTTTGNHFDANARAGMNNQGFY 179
120 TYDIYETTRYNAPSEVGRKTFQOYWSVRSKVTSSGSLTTTGNHFDANARAGMNNQGFY 179

QY 171 YQIYAVEGYFSSGSASITVS 190
171 YQIYAVEGYFSSGSASITVS 190
Db 180 YIMATEGYSSGSSSNTIVS 199
180 YIMATEGYSSGSSSNTIVS 199

RESULT 40
US-08-044-621D-33
Sequence 33, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Makarchuk
APPLICANT: Wang L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gowling, Strathly & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Erftelt

REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 189
TYPE: Amino Acid
STRANDEDNESS: No. 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No
ORIGINAL SOURCE:
ORGANISM: Streptomyces sp.
STRAIN: Streptomyces sp. #36a
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Nagashima M., Okumoto Y. & Okanishi M.
TITLE:
JOURNAL: Trends In Actinomycetologia
VOLUME:
ISSUE:
PAGES: 91-96
DATE: 1989
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-33

Query Match 50.8%; Score 531.5; DB 1; Length 189;
Best Local Similarity 52.1%; Pred. No. 4.1e-22;
Matches 99; Conservative 34; Mismatches 52; Indels 5; Caps 5;

QY 2 TTPGCTGYNNGYFYSYWNMGHGVITYTNGGQFYSVWMSNGNFVGKGNQPGTKKNVIN 61
DB 3 TTNETGY-DGMYTSFTDGGSVSMTLNCGGSYSTRWNCGNFVAGKGNANGR-RTVR 60
QY 62 FSGSYVNGNSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSYYDIYRQ 121
DB 61 YTGMPNPSGNGYCLGWTSPNPLEYIYVDNMGSYRP-TGETR-GTYHSDGTYDIYKT 118
QY 122 RVNOPSITGATFYQYVSVRRNHRSSGSVNTANHFNMAOQGLTGTMD-YQIYAVEGYF 180
DB 119 RYNAPSVLEAPALDQYVSVRSKVTSGTITTGHNHFDAMARAGNMGNFRYYIMATEGYQ 178
QY 181 SSGSASTVS 190
DB 179 SSGSSTIVS 188

RESULT 41
US-08-044-621D-35
Sequence 35, Application US/08044621D
GENERAL INFORMATION:
PATENT NO. 5405769
APPLICANT: Warren W. Makarchuk
APPLICANT: Ming L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gowling, Strathly & Henderson

STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Errell
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 191
TYPE: Amino Acid
STRANDEDNESS: No. 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No
ORIGINAL SOURCE:
ORGANISM: Streptomyces lividans
STRAIN: Streptomyces lividans, Xln C
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Shareck, F., Roy, C., Yaguchi, M.,
AUTHORS: Morosoli, R. & Kluepfel, D.
TITLE:
JOURNAL: Gene
VOLUME: 107
ISSUE:
PAGES: 75-82
DATE: 1991
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-35

Query Match 50.8%; Score 531; DB 1; Length 191;
Best Local Similarity 53.1%; Pred. No. 4.4e-22;
Matches 102; Conservative 30; Mismatches 50; Indels 10; Caps 6;

QY 2 TTPGCTGYNNGYFYSYWNMGHGVITYTNGGQFYSVWMSNGNFVGKGNQPGTKKNVIN 61
DB 6 TNGTGT---DGMYTSFTDGGSVSMTLNCGGSYSTWNCGNFVAGKGNSTGDN--VR 60
QY 62 FSGSYVNGNSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSYYDIYRQ 121
DB 61 YNGYFNPVNGYCLGWTSPNPLEYIYVDNMGSYRP-TGYR-GTVSSDGGTYDIYQT 118
QY 122 RVNOPSITGATFYQYVSVRRNHRSSGS--VNTANHFNMAOQGLTGTMD-YQIYAVEG 178
DB 119 RYNAPSVLEKTFQYVSVRSKVTSGTITTGHNHFDAMARAGNMGNFRYYIMATEG 178

OY 179 YFSSGSASITVS 190
I : : : : :
Db 179 YOSSGSNITVS 190

RESULT 42

US-08-709-912-12
Sequence 12, Application US/08709912
Patent No. 5759840

GENERAL INFORMATION:

APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912

FILING DATE: 09-SEP-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr., Warren E

REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 1039,2000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-2400

TELEFAX: (212) 758-2982

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 189 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: Streptomyces sp. 36a

PUBLICATION INFORMATION:

AUTHORS: Nagashima, M

AUTHORS: Okumoto, Y

AUTHORS: Okanishi, M

JOURNAL: Trends in Actinomycetologia

PAGES: 91-96

DATE: 1989

US-08-709-912-12

Query Match 50.7%; Score 529.5; DB 1: Length 189;

Best Local Similarity 51.6%; Pred. No. 5,2e-22;

Matches 98; Conservative 35; Mismatches 52; Indels 5; Gaps 5;

OY 2 TIOPTGVNNGYFYSWNDHGCVTYTNGPGGOFVSNMNSGPNFYGKGMQPGTKNKVIN 61

Db 3 TITNENGY-DGMYISPTDGGGSVMTLNGGGSYSFRMTNCGNPFPAKGMAGGR-RIVR 60

OY 62 FSGSINPNKNSLSTLYYGSNRNPLIEYIVENFGTINPSTGATKLGKLVYSDGSVIDIYTKQ 121

Db 61 YTGWNPSPSCNGYGLGYMTSNPLVEYIVDMNGSYRP-TGEMR-GTVHSDGGCTYDIYKTT 118

OY 122 RVNPSIIGTATFYQWVSRRNRSSGSYNTANHHFNANAQGLTGLTMDYOIV-AVEGVF 180
I : : : : :
Db 119 RYNAPSVEAPAFEDQYWSYRSKVTSGTITGNHFDANARAGMNGNFRYYMINATEGYQ 178

OY 181 SSGSASITVS 190
I : : : : :
Db 179 SSGSSNITVS 188

RESULT 43

US-09-047-370-12
Sequence 12, Application US/09047370
Patent No. 5866408

GENERAL INFORMATION:

APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/709,912

FILING DATE: 09-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr., Warren E

REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 1039,2000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-2400

TELEFAX: (212) 758-2982

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 189 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: Streptomyces sp. 36a

PUBLICATION INFORMATION:

AUTHORS: Nagashima, M

AUTHORS: Okumoto, Y

AUTHORS: Okanishi, M

JOURNAL: Trends in Actinomycetologia

PAGES: 91-96

DATE: 1989

US-09-047-370-12

Query Match 50.7%; Score 529.5; DB 2: Length 189;

Best Local Similarity 51.6%; Pred. No. 5,2e-22;

Matches 98; Conservative 35; Mismatches 52; Indels 5; Gaps 5;

OY 2 TIOPTGVNNGYFYSWNDHGCVTYTNGPGGOFVSNMNSGPNFYGKGMQPGTKNKVIN 61

Db 3 TITNMGY-DGMYSFMTDGGGSVMTLNGGGSYSTRTMNCNCFVAGKGMANGR-RTVR 60
QY 62 FGSYVNPNGNSLYSVGMSRNPLEYIYENFCTYVPSGATKRLGEVTSDDGSVYDIYRQ 121
Db 61 YGWFNPNGNGYGLGWTSNPLVEYIYDNNGSYRP-TGTER-GRVSHDGGTYDIYQTT 118
QY 122 RVNOPSITGATFYQYVSVRRNRRSSGSVNTANHFNAQAQGLTLGTMDYOIV-AVEGYE 180
Db 119 RVNAPVEEPAAFDQYVSVRSQSVTSCTITTGNHFDAMARAGNMGNFRYYMINATEGY 178
QY 181 SSGSASITVS 190
Db 179 SSGSSNITVS 188

RESULT 44
US-08-709-912-11
Sequence 11, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr., Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
STRAIN: xln C
ORGANISM: Streptomyces lividans
PUBLICATION INFORMATION:
AUTHORS: Shareck, F
AUTHORS: Roy, C
AUTHORS: Yaguchi, M
AUTHORS: Morosoli, R
AUTHORS: Kluepfel, D
JOURNAL: Gene
VOLUME: 107
PAGES: 75-82

DATE: 1991
US-08-709-912-11
Query Match 50.6%; Score 529; DB 1: Length 191;
Best Local Similarity 52.6%; Pred. No. 5, 7e-22;
Matches 101; Conservative 31; Mismatches 50; Indels 10; Gaps 6;

QY 2 TTPGTYNNGYFYVYNDGHGVYTNPGGQFSYVWMSNGNFVAGKGMOPGTNRKYN 61
Db 6 TNGTGT---DGMYSFMTDGGGSVMTLNGGGSYSTQMTNCGNCFVAGKGMSTGDCN--VR 60
QY 62 FGSYVNPNGNSLYSVGMSRNPLEYIYENFCTYVPSGATKRLGEVTSDDGSVYDIYRQ 121
Db 61 YGWFNPNGNGYGLGWTSNPLVEYIYDNNGSYRP-TGTER-GRVSHDGGTYDIYQTT 118
QY 122 RVNOPSITGATFYQYVSVRRNRRSSGS--VNTANHFNAQAQGLTLGTMDYOIV-AVEG 178
Db 119 RVNAPVEECPKFOQYVSVRSQSVTSCTITTGNHFDAMARAGNMGNFRYYMINATEG 178
QY 179 YFSSGSASITVS 190
Db 179 YOSSSSNITVS 190

RESULT 45
US-09-047-370-11
Sequence 11, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr., Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:

ORGANISM: Streptomyces lividans
STRAIN: xln C
PUBLICATION INFORMATION:
AUTHORS: Shareck, F
AUTHORS: Roy, C
AUTHORS: Taguchi, M
AUTHORS: Morosoli, R
AUTHORS: Kluepfel, D
JOURNAL: Gene
VOLUME: 107
PAGES: 75-82
DATE: 1991
US-09-047-370-11

Query Match
Best Local Similarity 52.6%; Score 529; DB 2; Length 191;
Matches 101; Conservative 31; Mismatches 50; Indels 10; Gaps 6;

QY 2 TTQGTGYNNGYFYSYWDGHCYVYTNCGGQFYSVMSNSGNFVGKGMQPTKKNKYN 61
DB 6 TNOTGT---DGMYSFMTDGGGVSMTLNGGGYSTQMTNCGNFVAGKGMSTGDCN--VR 60
QY 62 FGGSYRPNNSYLSYVGNRNPLIEYIYENFGTYNPSTGATKLGCVTSDGSVYDIYRTQ 121
DB 61 YNGYFNPVNGYGLGWTSMPLVEYIYDNNMGSTYR-TGYK-GTVSSDGGCTYDIYQTT 118
QY 122 RVNOPSITGATFYQYVSVRRNHRSSGS--VNTANHFNMAAQGLTGMTDYQIV-AVGG 178
DB 119 RYNAPSVECTKTFTQYVSVRSKRYTSGSGTITTGNNFDMARAGMMGCPRIYMINATGG 178
QY 179 YFSSGSASITVS 190
DB 179 YSSGSSNITVS 190

RESULT 46
US-08-104-445-3
Sequence 3, Application 08/104445
Patent No. 5306633
GENERAL INFORMATION:
APPLICANT: GOTTSCALK, MICHAEL
APPLICANT: SCHUSTER, ERWIN
APPLICANT: SPROESSLER, BRUNO
TITLE OF INVENTION: BACTERIAL XYLANASE, METHOD FOR ITS
TITLE OF INVENTION: PRODUCTION, BACTERIA PRODUCING A XYLANASE, DNA FRAGMENT
TITLE OF INVENTION: ENCODING A XYLANASE, PLASMID CONTAINING THE DNA FRAGMENT,
TITLE OF INVENTION: BAKING AGENTS CONTAINING A XYLANASE, AND METHOD FO
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/104,445
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 530663man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 583-179-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-104-445-3

Query Match
Best Local Similarity 49.1%; Score 512.7; DB 1; Length 213;
Matches 101; Conservative 28; Mismatches 48; Indels 13; Gaps 7;

QY 6 GTGYNNGYFYSYWDGHCYVYTNCGGQFYSVMSNSGNFVGKGMQPTKKNKYNF-SG 64
DB 30 GNDYD-----WQMTDCCGTFVNAVNSGCVSVMSMTGNFVVGKMTTSPRTINYNAG 84
QY 65 STPNPNSYLSYVGNRNPLIEYIYENFGTYNPSTGATKLGCVTSDGSVYDIYRTQRYN 124
DB 85 VVAPNNGYLTLYGWRSPLEIYVYVDSWGYRP-TGYK-GTVSSDGGCTYDIYTTTRYN 142
QY 125 OPSITG-TATFYQYVSVRRNHRSSGS--VNTANHFNMAAQGLTGMT-DYQIVAVEGY 179
DB 143 APSIDGNTTFTQYVSVRSKRYTSGSGTITTGNNFDMARAGMMGCPRIYMINATGG 202
QY 180 FSSGSASITV 189
DB 203 KSSGSSNITV 212

RESULT 47
US-09-189-060B-12
Sequence 12, Application US/09189060B
Patent No. 6270968
GENERAL INFORMATION:
APPLICANT: Dalboge, Henrik
APPLICANT: Sandel, Thomas
APPLICANT: Kauppinen, Markus
APPLICANT: Borge, Diderichsen
TITLE OF INVENTION: Method of Providing No. 6270968e1 DNA Sequences
FILE REFERENCE: 4772.204-US
CURRENT APPLICATION NUMBER: US/09/189,060B
CURRENT FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: PCT/DK97/00216
PRIOR FILING DATE: 1997-05-12
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 248
TYPE: PRT
ORGANISM: Hybrid
US-09-189-060B-12

Query Match
Best Local Similarity 48.5%; Score 506.5; DB 4; Length 248;
Matches 96; Conservative 32; Mismatches 52; Indels 25; Gaps 4;

QY 8 GYNNGYFYSYWDGHCYVYTNCGGQFYSVMSNSGNFVGKGMQPTKKNKYNF-SG 58
DB 36 GNDGTDYEFMKDGGSGTMTLLNHGTFSAQNNNNNNLLFRGKKFNETQTHQVG--NM 93
QY 59 VINFSGSYNPNNSYLSYVGNRNPLIEYIYENFGTYNPSTGATKLGCVTSDGSVYDIY 118
DB 94 STNYGANFOPNCGNATLYCVGWTVDPLVEYIYDMSGNMNP-PGATPKGCTITVDGCTYDIY 152
QY 119 RTQRYNOPSITGATFYQYVSVRRNHRSSGSVNTANHFNMAAQGLTGMTDYQIVAVEG 178
DB 153 KRDQVNPSTGATFYQYVSVRSKRYTSGSGTITTGNNFDMARAGMMGCPRIYMINATGG 212
QY 179 YFSSGSASITVS 190
DB 213 YOSTGSANVYSNTLRINGNPLSTIS 237

VOLUME: 144
PAGES: 201-206
DATE: 1986
US-08-709-912-5

Query Match 48.4%; Score 506.2; DB 1; Length 185;
Best Local Similarity 53.8%; Pred. No. 9, 6e-21;
Matches 98; Conservative 29; Mismatches 47; Indels 8; Gaps 6;

QY 14 FYSYNDGCGVYTTNGPGGFSVNMNSGNGFVGGKMGOPGTRKNKYINF-SGSYNPNGNS 72
DB 5 YWQNMWDGCGIYNAVAVNGSGGNTSVNMSNTGNFVVGKMTTGSFRTINYNAGVMAFNGNG 64
QY 73 YLSVYGSRNPLEIYIVENFGTYNPGTGATKLGVEYSDGSVYDIYRTORVNOPTIIG-T 131
DB 65 YLLVGMTRSPLEIYVVDVSMGTYRP-TGTYK-GTYKSDGTYDIYTTTRYNAPSIDGR 122
QY 132 ATFFQYWSVRRNHRSSGS---VNTANHFNAMAQGLTIGT-MDYQIVAVEGFSSGSASI 187
DB 123 TFFQYWSVRSKRPTGSNATITFSNHNAMKSHGNLGSNNMAYQVMATEGYQSSGSNNV 182
QY 188 TV 189
DB 183 TV 184

RESULT 50

US-09-047-370-5
Sequence 5, Application US/09047370
Patent No. 5866408

GENERAL INFORMATION:

APPLICANT: Sung Dr., Ming L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 1039,2000
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 185 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Bacillus subtilis
PUBLICATION INFORMATION:

AUTHORS: Parce, M.G.
AUTHORS: Bourdonnais, R
AUTHORS: Desrochers, M
AUTHORS: Jurassek, L
AUTHORS: Yaguchi, M
JOURNAL: Arch. Microbiol.

VOLUME: 144
PAGES: 201-206
DATE: 1986
US-09-047-370-5

Query Match 48.4%; Score 506.2; DB 2; Length 185;
Best Local Similarity 53.8%; Pred. No. 9, 6e-21;
Matches 98; Conservative 29; Mismatches 47; Indels 8; Gaps 6;

QY 14 FYSYNDGCGVYTTNGPGGFSVNMNSGNGFVGGKMGOPGTRKNKYINF-SGSYNPNGNS 72
DB 5 YWQNMWDGCGIYNAVAVNGSGGNTSVNMSNTGNFVVGKMTTGSFRTINYNAGVMAFNGNG 64
QY 73 YLSVYGSRNPLEIYIVENFGTYNPGTGATKLGVEYSDGSVYDIYRTORVNOPTIIG-T 131
DB 65 YLLVGMTRSPLEIYVVDVSMGTYRP-TGTYK-GTYKSDGTYDIYTTTRYNAPSIDGR 122
QY 132 ATFFQYWSVRRNHRSSGS---VNTANHFNAMAQGLTIGT-MDYQIVAVEGFSSGSASI 187
DB 123 TFFQYWSVRSKRPTGSNATITFSNHNAMKSHGNLGSNNMAYQVMATEGYQSSGSNNV 182
QY 188 TV 189
DB 183 TV 184

Search completed: July 1, 2003, 11:51:26
Job time : 30 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: July 1, 2003, 11:49:34 ; Search time 49 Seconds

(without alignments)
425.161 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045

Sequence: 1 OTIQPGTGNMGYFYSYMND.....YQIVAEYFSSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.1

Searched: 424699 seqs, 109646833 residues

Total number of hits satisfying chosen parameters: 424699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA.*
1: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	686.6	65.7	313	US-10-213-990-72	Sequence 72, Appl
2	677.5	64.8	234	US-10-213-990-69	Sequence 66, Appl
3	671.3	64.2	221	US-10-213-990-66	Sequence 66, Appl
4	647.9	62.0	223	US-10-299-393-2	Sequence 2, Appl
5	647.8	62.0	217	US-09-790-070A-11	Sequence 11, Appl
6	635.9	60.9	225	US-09-467-368-2	Sequence 2, Appl
7	597.5	57.2	344	US-09-770-621-2	Sequence 2, Appl
8	481.9	46.1	133	US-09-790-070A-10	Sequence 10, Appl
9	475.5	45.5	221	US-09-909-207-3	Sequence 3, Appl
10	475.5	45.5	248	US-09-909-207-6	Sequence 6, Appl
11	437	41.8	185	US-09-970-616-2	Sequence 2, Appl
12	177	16.9	84	US-09-790-070A-9	Sequence 9, Appl
13	153.7	14.9	776	US-09-833-435A-7	Sequence 7, Appl
14	153.7	14.7	776	US-09-833-435A-4	Sequence 4, Appl
15	143.8	13.8	726	US-10-155-400-7	Sequence 12, Appl
16	143	13.7	659	US-10-090-624-12	Sequence 364, App
17	142.2	13.6	878	US-09-912-020-364	Sequence 13, Appl
18	140.2	13.4	1436	US-10-080-505-13	Sequence 10132, A
19	139	13.3	729	US-09-815-242-10132	

20	138.7	13.3	1974	9	US-09-895-913A-12	Sequence 12, Appl
21	137.7	13.2	943	9	US-09-996-634-131	Sequence 131, App
22	137.7	13.2	943	9	US-09-997-181-131	Sequence 131, App
23	137.7	13.2	943	9	US-09-997-182-131	Sequence 131, App
24	136.3	13.0	793	10	US-09-881-752A-362	Sequence 362, App
25	135.7	13.0	957	9	US-10-155-400-1	Sequence 1, Appl
26	135.4	13.0	719	9	US-10-234-266-2	Sequence 2, Appl
27	134.8	12.9	956	9	US-10-121-032-63	Sequence 63, Appl
28	134.8	12.9	956	9	US-10-093-037-63	Sequence 63, Appl
29	133.6	12.8	1781	9	US-09-995-749A-2	Sequence 2, Appl
30	133	12.7	553	10	US-09-888-224-2	Sequence 2, Appl
31	132.9	12.7	400	9	US-09-797-464A-4	Sequence 4, Appl
32	132.7	12.7	1043	9	US-09-917-384-6	Sequence 6, Appl
33	132.7	12.7	1043	9	US-09-917-384-6	Sequence 6, Appl
34	132.2	12.7	1477	9	US-10-092-880-4	Sequence 4, Appl
35	131.9	12.6	700	10	US-09-841-132-345	Sequence 345, App
36	131.8	12.6	522	12	US-10-090-624-4	Sequence 4, Appl
37	131.8	12.6	654	12	US-10-090-624-16	Sequence 16, Appl
38	131.2	12.6	742	10	US-09-815-242-4989	Sequence 4989, Ap
39	131.2	12.6	742	10	US-09-815-242-10634	Sequence 10634, A
40	130.9	12.5	639	10	US-09-782-906-2	Sequence 2, Appl
41	130.9	12.5	639	10	US-09-782-906-3	Sequence 3, Appl
42	130.9	12.5	639	10	US-09-782-906-4	Sequence 4, Appl
43	130.9	12.5	639	10	US-09-782-906-5	Sequence 5, Appl
44	130.8	12.5	1325	10	US-09-741-669-304	Sequence 304, App
45	130.4	12.5	925	9	US-09-924-097-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-213-990-72
; Sequence 72, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Bussey, Howard
; APPLICANT: Bussey, Reg
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 313
; TYPE: PRN
; ORGANISM: Aspergillus
US-10-213-990-72

Query Match 65.7%; Score 686.6; DB 9; Length 313;
Best Local Similarity 64.2%; Pred. No. 1.4e-25;
Matches 124; Conservative 29; Mismatches 36; Indels 4; Gaps 3;

QY	1	OTIQPGTGNMGYFYSYMNDHCGVTTTNGGCGSFVMS--NSGNFVGKGNQPTKRN	57
DB	32	OTITTSQTCNTNGYYSFTNTAGSVQYTTNGAGGEYSVTMAWNGDFTCGKGNMPSGDH	91
QY	58	KVINFSGSYNPNGSNYLSVYCGWRNPLIEYIVENFGTYNPSTGATKJGEVYSDSDSYDI	117
DB	92	D-TTSSGSNPNCGNAYLSYGTTPPLEYITLLENYGSINPSSGNTHKGTIVSDSDYDI	150
QY	118	YTFQRYNPSITIGTATFYQYWSVRNRHSSGSVNTANFNMAQGLTLGTNDYOIVAVE	177
DB	151	YHQQVQNPSTIGTATFYQYWSVRNRHSSGSVNTANFNMAQGLTLGTNDYOIVAVE	210
QY	178	GYSSGSASITVS 190	
DB	211	GYSSGSSTITVS 223	

SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-770-621-2

Query Match 57.2%; Score 597.5; DB 10; Length 344;
Best Local Similarity 53.5%; Pred. No. 3e-21;
Matches 106; Conservative 35; Mismatches 42; Indels 15; Gaps 4;

QY 5 PGT-----GYNNGYFYSYNDGHCYTYNPGGQFVSVMNSGNEVGSKGMQ 52
DB 38 PGTAAHDTTITONQOTYDNGYFSEFTDAAGTVSMTLHSGSYSTSMRNTGNFVACKGMS 97
QY 53 PGTKNVINPSCGNSYLSYVGMNRNPLIEYIVENFGYNPSTGATKIGEVTSQG 112
DB 98 TGR-RTVYNASFNFGYGLTLGVTNRNPLIEYIVESWGYRP-TGYK-GVATTDG 154
QY 113 SYVDIYRTQVNOPSIIGTATFYQVSVRRNHRSSGSVNTANHFNAAOGLTLGTMDO 172
DB 155 GTYDIYETRYNAPSIEGTRTEQGFWSVQOKRTSGTITIGNHFDAMARAGMNLGSHDY 214
QY 173 IVAVEGFSSGSASTVS 190
DB 215 IMATEGYQSSGSTVSIS 232

RESULT 8

US-09-790-070A-10
Sequence 10, Application US/09790070A
Publication No. US20030053999A1
GENERAL INFORMATION:
APPLICANT: Jonnaux, Jean-Luc
APPLICANT: Dauvin, Thierry
TITLE OF INVENTION: ENZYME WITH XYLANASE ACTIVITY
FILE REFERENCE: VANM199.001AUS
CURRENT APPLICATION NUMBER: US/09/790,070A
CURRENT FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: EP 00870028.8
PRIOR FILING DATE: 2000-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 133
TYPE: PRT
ORGANISM: Penicillium griseofulvum
US-09-790-070A-10

Query Match 46.1%; Score 481.9; DB 9; Length 133;
Best Local Similarity 67.4%; Pred. No. 2.3e-16;
Matches 89; Conservative 20; Mismatches 22; Indels 1; Gaps 1;

QY 60 INFSGSYNPNNGNSYLSYVGMNRNPLIEYIVENFGYNPSTGATKIGEVTSQGVYDIYR 119
DB 2 INFSGFNFSNAGYLAIVGTMKPLVEYIMENYCGMTEFGTYSQGSVYDIYK 61
QY 120 TORVNOPSTIG-TATFYQVSVRRNHRSSGSVNTANHFNAAOGLTLGTMDOYQVAVEG 178
DB 62 HTQVNOPSTIISDSSTFDQVWIRNRKRSCTVTTGNHFNAAKLGMGLSHDYQVNTG 121
QY 179 YFSSGSASTVS 190
DB 122 YOSSGSASTIVS 133

RESULT 9

US-09-909-207-3
Sequence 3, Application US/09909207
Patent No. US20020115181A1
GENERAL INFORMATION:
APPLICANT: ANDREE LAHAYE
ERIC DE BUYL

PIERRE LEDOUX
RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced lt.
DNA molecule, processes for preparation of this xylanase
and uses thereof

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhelm F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-909-207-3

Query Match 45.5%; Score 475.5; DB 10; Length 221;
Best Local Similarity 45.4%; Pred. No. 1e-15;
Matches 93; Conservative 29; Mismatches 58; Indels 25; Gaps 4;

QY 8 GYNNGYFYSYNDGHCYTYNPGGQFVSVMNSGNEVGSKG-----WPGTKNK 58
DB 9 GNHDDYDFEWMKDSGSGTMIINHGTFSACMNNVNNILFRKGRFNETQHQVG--NM 66
QY 59 VINFSGSYNPNNGNSYLSYVGMNRNPLIEYIVENFGYNPSTGATKIGEVTSQGVYDIY 118
DB 67 STINGANFOPNNAVLGYGTVDPPLVEYIVDSMGMRP-PGATPKGTVVDGCTYDIY 125
QY 119 RTQVNOPSTIIGTATFYQVSVRRNHRSSGSVNTANHFNAAOGLTLGTMDOYQVAVEG 178
DB 126 ETLRVNOPSIKIGIAFYQVSVRRSKRTSGTISVNHFRAMENLGMNGKMEVALTYEG 185
QY 179 YFSSGSASTVS 190
DB 186 YOSSGSANYSNTRLINGNPLSTIS 210

RESULT 10

US-09-909-207-6
Sequence 6, Application US/09909207
Patent No. US20020115181A1
GENERAL INFORMATION:
APPLICANT: ANDREE LAHAYE
ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced lt.

Db 354 LTSGNOYFYDNTGICANENTYNTVAONLIVDSLAWANTMGVDFRDLASVLGNSCLNG 413
QY 98 -----PSGAT----- 103
Db 414 AVTASAPNCNGNVPDADSNVAINRILREFTVPAAGSGLDLFAEPMAIGNSYOLG 473
QY 104 -----KLGEXT----- 109
Db 414 GFRQGMSEMNGLFRSLRLQAOVELGSMITTYVIQDANDESGSSNLFOSSGRSPWNSINFID 533
QY 110 -SDG-SYVDYRTQRYNO-----PSIIGATFYQY----- 137
Db 534 VHDGMTLKDYSKNCANNNSQAMPYGPSPDGGTSTNYSWDQGSAGTGAVDQRAARTGMA 593
QY 138 -----MSV-----RR 142
Db 594 FEMLSAGTPLMGDEYLTFTLOCCNNNAVNLDSANMLTYSWTTDOSNEFYTAQRLIAFRK 653
QY 143 NH-----RSSGSV-----NTANHEFMAAOGLTGTMDYQIVAVEG 178
Db 654 AHPALRPSSWYSGSOLTWYQPSGAVADSNYMNNTSNALAYAINGPSLGDNSIYVAING 713
QY 179 YFSSGSASIT 188
Db 714 W-----SSSVT 719

RESULT 15

US-10-155-400-7
; Sequence 7, Application US/10155400
; Publication No. US20030108988A1
; GENERAL INFORMATION:
; APPLICANT: DING, SHI-YOU
; APPLICANT: ADNEY, WILLIAM S.
; APPLICANT: VINZANT, TODD B.
; APPLICANT: HIMMEL, MICHAEL E.
; TITLE OF INVENTION: THERMAL TOLERANT AVICELASE FROM ACIDOTHERMUS
; FILE REFERENCE: NREL 01-36A
; CURRENT APPLICATION NUMBER: US/10/155,400
; CURRENT FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 726
; TYPE: prt
; ORGANISM: Aspergillus aculeatus
US-10-155-400-7

Query Match 13.8%: Score 143.8; DB 9: Length 726;
Best Local Similarity 12.3%: Pred. No. 57;
Matches 72: Conservative 27; Mismatches 73; Indels 412; Gaps 21;

QY 5 PCTGY-----NNGYFYSYWNDGHC-----GVTYT 28
Db 123 PERGGERLAVDPKNKNSILYFCARGHGLMKSTVDGATWSNVSFTWTCTYFQDSSSTYT 182
QY 29 NCPGGOFSYNN-----SNSGN-----FVG-----GKGN----- 51
Db 183 SDPVG-----IAWTFPDSTSGSSGSATPRIFGVADAGKSVKSEDAAGATWAMVSGEPQYGF 239
QY 52 -----QPGTKNKYINFSGSYNP----- 68
Db 240 LPHKGVLSPEKTLTYISTANGAGPYDGTNGTVHKNTISGVTWTDISPSTSLASTYGYGGL 299
QY 69 -----NGNSYLSYVGYMSRNPLEY----- 88
Db 300 SVDLOVPGTLVVAALNCMMWPDLLFRSTDSGATNSPIMEMNGPSINITYSIDISNAPVI 359
QY 89 -----IVEN----- 92
Db 360 QDTTSDQFPVAVGMVVEALAIIDPDSNHLTYGTLTYGCHDLTNMDSKHNVTVSLAV 419

QY 93 -----FGYVNPSTGATKLGEXTSDGSY-----DIYRTQRY-----NQP 126
Db 420 GIEEMAVUGLITTPGGPALLSAVDDGCFYHSDLDAPNQAHTFYCTTGWIDYAGNKP 479
QY 127 SII----- 129
Db 480 SNIVSGASDDYPTLALSNGSTWYADYASTGTGTGAVALSADGDTVLLMSSTSGALV 539
QY 130 -----GTAT-----FYQYWSVRNRHRSGSV-----NTANHE----- 156
Db 540 SKSQGTPLAVSSLPSCAVIASDKSDNTVEY-----GGSAGAIYVSKMTATSTKTVS 591
QY 157 -----NANAQ-----QGLTLG----- 167
Db 592 LGSSTTVNAIRHPSIADGWMASTDKGLMHSSTDGSTFTQIGSGVTAGMSEFGKASSTG 651
QY 168 -----TMD-----YOIVAVEGY-FSSGSASI 187
Db 652 SYVVIYGFFTIDGAGLFRKSEDAAGTNMQVYISDASHGFGSGSANV 695

RESULT 16

US-10-090-624-12
; Sequence 12, Application US/10090624
; Patent No. US20020132335A1
; GENERAL INFORMATION:
; APPLICANT: TAKAKURA, Hikaru
; APPLICANT: MORISHITA, Mio
; APPLICANT: SHIMOJO, Tomoko
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunosbin
; TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
; FILE REFERENCE: TAKAKURA-6
; CURRENT APPLICATION NUMBER: US/10/090,624
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/445,472
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 151969/1997
; PRIOR FILING DATE: 1997-06-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 659
; TYPE: prt
; ORGANISM: Thermococcus celer
US-10-090-624-12

Query Match 13.7%: Score 143; DB 12: Length 659;
Best Local Similarity 12.2%: Pred. No. 53;
Matches 67: Conservative 22; Mismatches 50; Indels 410; Gaps 18;

QY 2 TTPCTGYN-----NCGYFSYWNDGHC-----GVT 26
Db 149 TWVNSLGYDGSVVVAIVDTGIDANHPDLKKGIVGMDAYVNGRSTPYDDOGHTVAGIV 208
QY 27 YTNG-----PGGQF-----SVNN----- 39
Db 209 ACTGSVQYIGVAGKALVGVKYLGDAGSGSVSTIAGVDMVYONKQYGRIVNLISLG 268
QY 40 -----SNSG----- 43
Db 269 SSQSSDGTDSLQAVNMMADAGIYVCVAAGNSGPTTYVGSPPAASKVITYCAVDSNDNI 328
QY 44 -----NFVSGKG 50
Db 329 ASESRCPTADRLKPEVAVPCVDIIPRASCTSMGTPINDYTTKASGTSMATPHVSGVG 388
QY 51 -----WPGTKNKY-----INF 62
Db 389 ALIIQAHPSWTP--DKVKTALITETADIYAPKEIADIYAGGRVNVYKAIKYDDYAKLTF 445
QY 63 SGS-----YNPNCN-----SYLSYVGWGRN 82

Db 446 TGSVADKGSATHTFDVSGATFTATLYMDTGSSDIDLTYDPNGNEVDYATAYGF--- 502
QY 83 PLEIYIVENFGTYNP----- 98
Db 503 -----EKVGYNPAGTWTYKVVSYKGAANYQDVVSDGSLSGCGGNPNPNPNP 554
QY 99 -----STGATKL-GEVTSDSGSVDI----- 117
Db 555 TPTTDTQTFNGSVNDYMDTSDFTMNVNSGATKITGDLTFDTSYNDLDTLYDPNGNLVD 614
QY 118 -----YRTQRYNOSIITATFTFYQVSVRRNHRSSGSVNTANHFMAOQGLTIGTMD 170
Db 615 RSTSSSYEHVEYANPA-PGTWTFLYV-----AYS-----TYGWAD 649
QY 171 YOIYAVEGY 179
Db 650 YOLKAVVY 658

RESULT 17
US-09-912-020-364
Sequence 364, Application US/09912020
Patent No. US20020045592A1
GENERAL INFORMATION:
APPLICANT: Zyskind, Judith
APPLICANT: Ohlsen, Karl L.
APPLICANT: Trawick, John
APPLICANT: Forsyth, R. Allyn
APPLICANT: Froelich, Jamie M.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
FILE REFERENCE: ELITRA.001DVI
CURRENT APPLICATION NUMBER: US/09/912.020
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 364
LENGTH: 878
TYPE: PRT
ORGANISM: E. coli
US-09-912-020-364

Query Match 13.6%; Score 142.2; DB 10; Length 878;
Best Local Similarity 16.2%; Pred. No. 92;
Matches 51; Conservative 20; Mismatches 46; Indels 198; Gaps 12;
QY 1 QTIQPGTGY-----NNGIFYSTWMDGHGCVTYTNGPG----- 32
Db 71 QELPQGT-YRVDIYLNNGYMAT-----RDVTFNTGDSGEGIVPCLTRAQLASMGINTAS 123
QY 33 -----GQFSYVMSNSGTFYVGKG-----WQPTK 56
Db 124 VAGMNLADDAVCPLTTMWDATAHLDVGQRLNLTPQAFMSNRARGVPPPELMDPGIN 183
QY 57 NKVINFSGSYNPNNGSYLSVYGMSRNPLEYIYVENFGTYNPSTGATKLGEVTSDSVD 116
Db 184 AGLLN-----YNFSGNS-----VQN----- 198
QY 117 IYRTQRYNOSIITATFTFYQVSVRRNHRSSGSVNTANHF 157
Db 199 -----RIGGSHVAYLMLQSGNLIGAWRLRDNTWTSYSSDRSSGSKNKWOHIN 247
QY 158 AMAOQ-----LTIGTMDYQIVAVEGY----- 179
Db 248 TWLERDIILRSRLTUG-----DGYTQGDIFDGINFGAQLASDDNMLPDSQGF 298

QY 180 -----FSSGSASTV 189
Db 299 PVIHGIARGTAYTI 313
RESULT 18
US-10-080-505-13
Sequence 13, Application US/10080505
Publication No. US20030073166A1
GENERAL INFORMATION:
APPLICANT: St. Geme, Joseph W.
TITLE OF INVENTION: HAEMOPHILUS ADHERENCE AND PENETRATION PROTEINS
FILE REFERENCE: A-59941-1/PRT/DCF/DHR
CURRENT APPLICATION NUMBER: US/10/080,505
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: US 08/296,791
PRIOR FILING DATE: 1994-10-25
PRIOR APPLICATION NUMBER: US 09/839,996
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 1436
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-10-080-505-13

Query Match 13.4%; Score 140.2; DB 9; Length 1436;
Best Local Similarity 9.5%; Pred. No. 2,5e+02;
Matches 70; Conservative 30; Mismatches 52; Indels 588; Gaps 22;

QY 1 QTIQPGTYNNGY-----FYSYW--NDGHGCVTYT- 29
Db 269 QTSNPFSGANGFQILRKMFIDNVVEDLPITFLEPRNSGHTSFTSNNGTGTYTQTN 328
QY 30 ----- 29
Db 329 KVSMPQKRYTVQLFNEALKEKDEPVYAAGVNAKPRLLNKNKTYFGDGTLTLEN 388
QY 30 -----GFGQF-----SYNMSNSGPNV-----GKC----- 50
Db 389 NINOGAGGLYFEGNFTVSSENNATWOGAGVHGEDSTVYKVGVEHRLSKIGKGLAI 448
QY 51 ----- 50
Db 449 QAKGENLGSIVDGKVIILDDQADENNOKAKREKIVSGRATVOLNSADVDPNNTYFC 508
QY 51 -----WQPTKRY--INF 62
Db 509 FRGRLDLNGSLTFKRIQNTDEGAMIVNHNTQVANITITGNESTAPSKNNKINIKLDY 568
QY 63 SG--SYNPNNGSYLSVYGMSRNPLEYIYVENFG-----TNPST----- 100
Db 569 SKELIAYN-----GW-----FGETDENKHKGRLLIYKPTTEDRTLL 605
QY 101 -GATKL-GEVTSDSG-----VDIYRTQRYNOSIIG-----TATF 134
Db 606 SCGTNLKGNITQBGGLVFSGRTPHAYN-----HLNRENELRPGGEVVIDDDMITRF 660
QY 135 ----YQY-----MSVRRNHR----- 146
Db 661 KAENFQIKGSAAVSRNVSISIEGNTVSNMNAAFGVNPNQNTICTRSDMTGLTTCYV 720
QY 147 ----- 150
Db 721 DLDTKVINSLPTTQINGSLNLTDNATVINIGLAKLNGVTLINHSQFTLSNNATQGTGNI 780
QY 151 NTAHNFNA----- 161
Db 781 QLSNHNATVDNANLNGVNLITDSAOFLKNSHFHQIOGDKCTTYTLENATWTMPSDAT 840
QY 162 -GGLT----- 166

Db 841 LONLTLNLTSTVTLNSAYSASANNAPRRSRLETTPTSAEHRFTLTVNGKLSGCTEQ 900
167 ----- 166
QY 901 FTSSLECYKSKDKLKSNDAGDYTLNRTNGKEPEALEQLTVESKDNKPLSDKIKFTLE 960
Db 167 -----GTMDYOIVAVEGYF 180
961 NDHVDAGALRYKLVKNNGEF 980

RESULT 19
US-09-815-242-10132
Sequence 10132, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10132
LENGTH: 729
TYPE: PRF
ORGANISM: Escherichia coli
US-09-815-242-10132

Query Match 13.3%; Score 139; DB 10; Length 729;
Best Local Similarity 14.1%; Pred. No. 98;
Matches 73; Conservative 20; Mismatches 70; Indels 353; Gaps 19;

QY 8 GYNN-----CYEYS-----YNN-DG- 21
227 GTONDSWLDRYNSEKTFEFGIVADADLGLTTLASGEYORIDVNSPTWGLPRMWTDS 286
QY 22 -----HGV-----TYT 28
287 SMSYDARSTAPDMAYNDKEINKVEMTLKQFADTQATLNNATHSEVEDSKMYVDAYV 346
QY 29 NCGPGGFSYNNWSNG---NFVGKGQWPGTKNKV-----INFGSY 66
347 NADAGLVGYPYSNYGPGFDYVGTGWNNG-KKRVADALDLFADGSYELFGROHLMFGSY 405
QY 67 NNNGNSYLSVYG-----WSKNPLIE----- 86
406 SKONNRYFSSMANIPDELIGSFYNNNGNFPOTDWSQSLAODDTTHMKSLYATRTVLAD 465
QY 87 -----YIVENFGTYNPST----- 100

Db 466 PLHLIGARYTNMRYDTLTYSMEKNHTTPEAGLVEDINDNMSTYASTSIFQPNDRDSS 525
101 ----- 100
QY 526 GRYLAPITGNMYELGKSDMNSRLTTLAIFRIEDQVNAOSTGPIPGSNGETA VKAVD 585
Db 101 -----GATK-----LGE 107
586 GTVSKGVERELNGALITDNNQLTFGATRYIAEDNEGNAVNPPLPTTVKMTSRYLVPME 645
QY 108 VTSDSGV-----YDIYRORYNOPS--IIGATPYQYWSVRNRHSSGSYVTANH 155
646 LTVGGVNMQRVYTDVTPYGTFRAGQGSYALVDLFTRYQ---VTKNFSLOGNVN--NL 700
QY 156 FNAMAQOGLTGTMDYOIVAVEG---YSSGSASIT 188
701 FDK-----TYD---TNVEGSIVYGTPRNFSIT 724

RESULT 20
US-09-895-913A-12
Sequence 12, Application US/09895913A
Patent No. US20020160456A1
GENERAL INFORMATION:
APPLICANT: Kleantous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean Francois
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
FILE OF INVENTION: Encoding No. US20020160456A1a1 Helicobacter Polypeptides in t
FILE REFERENCE: 06132/043002
CURRENT APPLICATION NUMBER: US/09/895,913A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 08/881,227
PRIOR FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 1974
TYPE: PRF
ORGANISM: Helicobacter pylori
US-09-895-913A-12

Query Match 13.3%; Score 138.7; DB 9; Length 1974;
Best Local Similarity 12.1%; Pred. No. 5e+02;
Matches 67; Conservative 34; Mismatches 78; Indels 373; Gaps 17;

QY 4 QPGTGNNNGYFYSYND-----GHGCVYTN-GPGGFS---YNNWSNG----- 43
342 QOTALENASSLSFYNNSVANFNNGTTAFNGVSYLNLNPAOVSEFNQVNNANVTFFYGLP 401
QY 44 -----NFVGKGQWPGTKNKVINFSG----- 64
402 LFGKTPDFGNSARLINFKNQTNFNQATLNLRAKHINHINQGVSTFKONSTMLAESSQAS 461
QY 65 -----SYNPNQNSYLSVYGWS-RNPLEYIVYVENFGTYNPSTGATKLGCVTSDG- 112
462 FNAKVEGETNFNLNSSILNFNNGSVFNAPVSFY-----ANHSQISFTKLATFNSDAS 515
QY 113 ----- 112
516 FDLNNSTLNFSOSVLLNGALNLLGNSNNLAINAKGNFSFGSKGILNLSYNNLFGDKKT 575
QY 113 SYVDIYRTORVN----- 124
576 SVYDVLQAOINIGLMMNNNGYEKIRFYGIQIDKADYSFDNGVHSWRTFNPLNTTETITL 635
QY 125 -----QPSIIG-----TATFYQWS-----V 140
636 HNNRLKVOISONGVSNKMFNLAPSLDYOKNPYNTEFNSYNTSDKVGTYVLTLSNKG 695

[illegible]

```

RESULT 21
US-09-996-634-131
Sequence 131, Application US/09996634
Patent No. US20020172684A1
GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
FILE OF INVENTION: Immunostimulatory Peptides
FILE REFERENCE: 61260
CURRENT APPLICATION NUMBER: US/09/996,634
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 131
LENGTH: 943
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-996-634-131

```

Query Match	13.2%	Score 137.7	DB: 9	Length 943:
Best Local Similarity	25.6%	Pred. No. 1.7e+02:		
Matches	58:	Conservative 14:	Mismatches 42:	Indels 113: Gaps 16:

OY	3	IQPCTGYNNNGYFYS-----	YWMDHGCGVTTYTNGPG-----	-GQFSVMWENS	42
Db	279	LNSTGTG-NIGLFENSGCTGVN	IGNSGCTGCMGICGNSGNSYNT	FGTNGSGDANTGFENNGIANT	337
OY	43	GNFPGGKGMQOCTANKKIYNF-	SGSYNPNGNSYLSVYGMSRNP	LEIYIVENFGTYNPSTG	101
Db	338	G--VGNAG-----	NNTGTGSYNP-GSNANTGCF	-----NMGOYN--TG	368
OY	102	ATKLGVEYSDGSVYDIYRTQ	RVFNQPSIIIGTATFYQYMSV	RRHRSSGSVNT---ANHN	157
Db	369	YLNSGN-----	YNTGLAN-----	SCWNVNCAFITGNFN	396
OY	158	---AMA---OQCLTGTDYQ	IVAVEGFSS-----	-----GSAS	186
Db	397	NGFLMRGDHQLIGFS-----	PGFENITSAPSSCFN	SAGDASAS	435

RESULT 22
US-09-997-181-131
: Sequence 131, Application US/09997181
: Publication NO. US20030049269A1
GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding

```

? TITLE OF INVENTION: Immunostimulatory Peptides
? FILE REFERENCE: 61257
? CURRENT APPLICATION NUMBER: US/09/997,181
? CURRENT FILING DATE: 2001-11-28
? PRIOR APPLICATION NUMBER: 09/447,135
? PRIOR FILING DATE: 2000-01-03
? PRIOR APPLICATION NUMBER: 08/990,823
? PRIOR FILING DATE: 1997-12-15
? PRIOR APPLICATION NUMBER: US 96/10375
? PRIOR FILING DATE: 1996-06-14
? PRIOR APPLICATION NUMBER: 60/000,254
? PRIOR FILING DATE: 1995-06-15
? NUMBER OF SEQ ID NOS: 169
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 131
? LENGTH: 943
? TYPE: PRT
? ORGANISM: Mycobacterium tuberculosis
? US-09-997-181-131

```

	Query Match	13.2%	Score 137.7	DB 9	Length 943
	Best Local Similarity	25.6%	Pred No. 1.7e+02		
	Matches	58:	Conservative 14:	Mismatches 42:	Indels 113: Gaps 16:
OY	3	IQPTGYNNGYFS-----	YVNDHGAGVTYTPG-----	GQFVSVMNS	42
Db					
	279	LNSGTG-IIGLEFNSTGTVNGISNQTGMGICNSGNSINTGFNGSGDANTGFNSGIANT			337
OY	43	GNFPGKMGMOGCTNKKNKYNF-SGSVPNPNGSNLYLSYGSRNPLEYTYIVEMFGYYNPSTG			101
Db					
	338	G-VGNAC-----NYNTGSTNP-GNSNTGCF-----NMGIN-TG			368
OY	102	ATKLGEVTSDSVDYIPIRQRNOPSLIGTATFYQYSVRNRHRSQGVNF----	ANHN		157
Db					
	369	YLNSGN-----YNTGLAN-----SCHWNTCAFITGMFN			396
OY	158	---AMA--QQGLTLGTMDYQIVAVEGYSS-----GSAS			186
Db					
	397	NGFLMRGDHGLIFGS-----PGEFNSTADPSGGFFNSGASGAS			435

```

RESULT 23
US-09-997-182-131
: Sequence 131, Application US/09997182
: Publication No. US20030049263A1
: GENERAL INFORMATION:
: APPLICANT: Nano, Francis
: TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
: TITLE OF INVENTION: immunostimulatory Peptides
: FILE REFERENCE: 61258
: CURRENT APPLICATION NUMBER: US/09/997,182
: PRIOR FILING DATE: 2001-11-28
: PRIOR APPLICATION NUMBER: 09/447,135
: PRIOR FILING DATE: 2000-01-03
: PRIOR APPLICATION NUMBER: 08/990, 823
: PRIOR FILING DATE: 1997-12-15
: PRIOR APPLICATION NUMBER: US 96/10375
: PRIOR FILING DATE: 1996-06-14
: PRIOR APPLICATION NUMBER: 60/000,254
: PRIOR FILING DATE: 1995-06-15
: NUMBER OF SEQ ID NOS: 169
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 131
: LENGTH: 943
: TYPE: PRT
: ORGANISM: Mycobacterium tuberculosis
US-09-997-182-131

```

```

Query Match      13.2%, Score 137.7; DB 9; Length 943;
Best Local Similarity 25.6%; Pred No. 1.7e+02;
Matches 58; Conservative 14; Mismatches 42; Indels 113; Gaps 16;

0y      3 IQPDTGNNNGIFY-----YANDHGCGVYTTNPG-----GQFVNMNSN 42

```

Db 279 LNSGTG-NIGLFNSGTGAVGICNSGTGMMGICNSGNSYNTGFGNSGDANTGFFNSGIANT 337
OY 43 GNFVGKMGQGTCKNKVINF-SGSYNPNNGSYLSTYGGSRNPLEYIVENPGTYNPSTG 101
Db 338 G-VGNAG-----NYNTGSYNP-GNSNTGCF-----MMGOYN--TG 368
OY 102 ATKLGEEVSDGSVDYDRTQORVNOPSLTGATFYQYWSRRNHRSSGSVNT---ANHFN 157
Db 369 YLNSGN-----YNTGLAN-----SGNVNTGAPITGNFN 396
OY 158 ---AWA--QGGLTGTMDYQIVAVEGYFS-----GSAS 186
Db 397 NGFLMRGDHQCILFGS-----PGFFNSTSAPSSGFFNSGAGSAS 435

RESULT 24
US-09-881-752A-362
Sequence 362, Application US/09881752A
Patent No. US20020115078A1
GENERAL INFORMATION:
APPLICANT: Kleantous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Francois
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of polynucleotides
TITLE OF INVENTION: Encoding No. US20020115078A1 Helicobacter Polypeptides in the
FILE OF INVENTION: Genome
FILE REFERENCE: 06132/041002
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/833,457
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 370
SOFTWARE: fastseq for windows version 4.0
SEQ ID NO 362
LENGTH: 793
TYPE: PRT
ORGANISM: Helicobacter pylori
US-09-881-752A-362

Query Match 13.0%; Score 136.3; DB 10; Length 793;
Best Local Similarity 11.1%; Pred. No. 1.5e+02;
Matches 59; Conservative 31; Mismatches 66; Indels 377; Gaps 16;

OY 5 PG-----TGTCNGCYFYSYWNGH----- 22
Db 96 PGQIRDATGTGVLPKISVRGFGG-----GNGHSNTMILVNGIPYGA PYSNIEAI 149
OY 23 -----GGVYTYNGP-----GGQFSY-----MNSN----- 41
Db 150 FPPVTFQSVDRIDVTKGTSVQYGPMTFGGVNITTKETPKREWENQAAERITFWGRSSGN 209
OY 42 -----SGNFVGGKMGQGTCKNKVINF 62
Db 210 FVDPREKPKPLAQTLGNQMLFNTYGRTAGMLGKHGISAQGWINGQGFQNSPTKQVNY 269
OY 63 -----SGSYNPN----- 69
Db 270 LLDVAYKINATNTFKAYYQYYQYNSYHPTLSAODYANRFINERPDNDGGRAKRFGIV 329
OY 70 -----GNSLYSYGMSRNLLEYIYVENGTYPN 98
Db 330 YQNTFGDPDRKVGDFKFTYTHDMSRDPGFSNOYQSYWSSQNKILPFKKGKISATNP 389
OY 99 STG-----ATKLGEEVSDGSV-----YDIYR- 119
Db 390 NCGLSTSYSDTNSPCQGFQNDIRRSVYNAPEPKLNIIVMTGKVKQTFNNMGMRFLTEDLYR 449
OY 120 ----- 119
Db 450 STTRKPSMPNNGSGFDAGTSLNPNFNNTAVYASDEINFNNGMLITPGLRYTFLNVEKK 509

OY 120 -----TORVNO-----PSIIGTA 132
Db 510 DAPPEKAGQGTGKTIKDRINQNNPRAVNVGKRIKELLFYFNQRSYIPPOFSNIGSVOTS 569
OY 133 T-FYQYWSVRNRNHRSSGS---VNTANHNMAAQGLTGLTMDYQIVAVEGYFS 181
Db 570 TDYQFQIFNV-----MEGGSRYEYFNNOVSFNA-----NYFVIFANNYFT 607

RESULT 25
US-10-155-400-1
Sequence 1, Application US/10155400
Publication No. US20030108988A1
GENERAL INFORMATION:
APPLICANT: DING, SHI-YOU
APPLICANT: ADNEY, WILLIAM S.
APPLICANT: VINZANT, TODD B.
APPLICANT: HIMMEL, MICHAEL E.
TITLE OF INVENTION: THERMAL TOLERANT AVICELASE FROM ACIDOTHERMUS
FILE REFERENCE: NREL 01-36A
CURRENT APPLICATION NUMBER: US/10/155,400
CURRENT FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 957
TYPE: PRT
ORGANISM: Acidothermus cellulolyticus
FEATURE:
NAME/KEY: MOD.RES
LOCATION: (957)
OTHER INFORMATION: Any amino acid
US-10-155-400-1

Query Match 13.0%; Score 135.7; DB 9; Length 957;
Best Local Similarity 9.9%; Pred. No. 2.2e+02;
Matches 75; Conservative 33; Mismatches 73; Indels 573; Gaps 22;

OY 2 TIQP-----GTGYNNGYFYSY-----WN 19
Db 48 TTQPYTWSNVAIGCGFVDGIIVFNEGAPGILYVRTDIGMYRMDANGRMIPLLDMWGMN 107
OY 20 D-GHCGV-----YTN----- 29
Db 108 NWGTNGVSIADAPINTNKVAAVGMVNTNSWDPNDGAILRSSDQATWQITPLPKLGN 167
OY 30 -----GPGQFSYN-----WSNCGNFV----- 46
Db 168 MPGRGMGERLAVDPNDNDILFPGAPSGKGLMRSTDSCATWQGMNFPDVGTYIANPTDTT 227
OY 47 -----CGKGMQ---PGTKNKVI 60
Db 228 GYQSDIQGVVWVAFDSSSSSLGQASKTIFGVADPNPNPFWMSRDGATWQAVCAPGTGFI 287
OY 61 NFSSGSYN-----NGNSYLSVY 77
Db 288 PHKGVDFVNVHLYIATSNTGOPYDGSSGDVWKFESVTSGMTIRISPVSDTDANDYFGYS 347
OY 78 G-----WSR----- 81
Db 348 GLTIDRHPNTIMATQISMWPDITIFRSTDOGATWMTIMDWTSYPNRSKRYVLDISAP 407
OY 82 -----NP----- 83
Db 408 WLTFGVQNPVPSPKLGMDMEAMAIIDPFNSDRMLYGTATLYATNDTLTKWDSGOIHIA 467
OY 84 -----LIEY- 87
Db 468 PMVGLLEETAVNDLISPPSAPLISALDLCGFTHADVTAVPSTIFTSPPVFTTGSVDYA 527
OY 88 ---YIVENFGTYNPST-----GATKLGVE--TSNGS----- 113

Db 528 ELNPSIIVRAGSFDPSOPDRHVAESTDCKNMFOGSEPCGYTGTGTVAAASADGSRFW 587
114 -----YVDI-----YRQRYNOPSI--IGTATPQ-----YV 138
Db 588 APDPCOPPVYAAVGFNSMAASGVPANAOIRSDRVNPKTFVALSNGETFRSTDDGVTQ 647
139 SVARNHRSSGSVYNTANH----- 155
Db 648 PVAAGLPSSGAVGVMFHAPGKEGDLMLAASSGLYHSTNGSSMSAITGVSSAVNNGFCR 707
156 -----FNMAQ----- 161
Db 708 SAPGSSYPAVFVGTIGVYTGAYRSDCGTTWVLINDDOHQYGMCAITGDHANERVY 767
162 -----OGLTGTMDYQIVAVEGFEFGSSASITVS 190
Db 768 IGTNGRGIVGDI-----GGAPSGSPSPSVS 793

RESULT 26

US-10-234-266-2
; Sequence 2, Application US/10234266
; Publication No. US2003005902A1
; GENERAL INFORMATION:
; APPLICANT: Chertey, Joel
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Beier, Lars
; APPLICANT: Frandsen, Torben
; APPLICANT: Schaefer, Thomas
; TITLE OF INVENTION: Amylolytic Enzyme Variants
; FILE REFERENCE: 5241.204-US
; CURRENT APPLICATION NUMBER: US/10/234,266
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US/09/645,707
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PRN
; ORGANISM: Bacillus sp.
US-10-234-266-2

Query Match 13.0%; Score 135.4; DB 9; Length 719;
Best Local Similarity 12.2%; Pred. No. 1.4e+02;
Matches 76; Conservative 26; Mismatches 57; Indels 466; Gaps 26;

QY 8 GYNGCYFYYSYV-----NDGH----- 22
Db 116 GTDNTGCHGWTRDFQIEHFGNMWTFPTLVNDAHQNGIKVIVDFVPHNSTPFKANDST 175
QY 23 ---GCVTYTNGP-----GGSFVSNN----- 40
Db 176 FAEGGALYNNGTVMGYFPDQATGYFHHNGDIS--NMDDRYEAOQKNFTDPAGESLADLQ 234
QY 41 -----NSG-----NFVCGK--GMO 52
Db 235 ENGTIOYLTDAVOLVANGADCLRIDAVKHFNSGSKSLADKLKQKDIPLVGEWYGD 294
QY 53 PGTKN-----KVINS-----GSY-----NPNNGSY----- 73
Db 295 PGTAHLEKRYRANNSGVVLDLDTVIRNVEGFTTQIMYDLMNNVNOTGNFYKKKENL 354
QY 74 -----LSV----- 76
Db 355 ITFIDNHDMSRFLSVNSKRALHQAFLILTSRGTPIYYTEQYVAGGNDPYNRGMPA 414
QY 77 -----YG-----WSRNPLEY----- 87
Db 415 PFTTTTAFKEVSTLAGLRNNNAIOYGTTRQWINDVYIERKFFNDVLAIVNNTOS 474

QY 88 -YIVENGT-----YNPSTGATKL 105
Db 475 SVSISGLQTAHPGASVADYLSGLLGGNGISVNSGASVFTLAPGAVSWOYISASAPQI 534
QY 106 GE-----VTSDGSYVDIYRQRYNOPSITATP----- 134
Db 535 GSVAIPNMGIPGNVNTIDKGFQ--TTQ-----GTVFQGVATVKSMTSRIEYVP 584
QY 135 -----YQY----- 137
Db 585 NMAAGLTDVKVYVAGVSNLSTYNILSGTQTSVFTVKSAPPYNIQDKIYLTGNIPELQ 644
QY 138 WSVARNHRSSGSVYNTAN-----HFNAM-----AOGGLT-----GTMDOIVAV 176
Db 645 WST-----DTSGAANNAGPLAPNPDPWFYVFSVPAGKTIQKFKIKRADGTIQME----- 696
QY 177 EGYFSSGS-----ASITVS 190
Db 697 -----NGSNHVATTPYGATGNITVT 716

RESULT 27

US-10-121-032-63
; Sequence 63, Application US/10121032
; Patent No. US20020155550A1
; GENERAL INFORMATION:
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/121,032
; FILING DATE: 09-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-Aug-1998
; APPLICATION NUMBER: 08/949,026
; FILING DATE: 10-Oct-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-Dec-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/024002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858/677-1456
; TELEFAX: 858/677-1465
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 956 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-121-032-63

Query Match 12.9%; Score 134.8; DB 9; Length 956;
Best Local Similarity 13.1%; Pred. No. 2.4e+02;
Matches 63; Conservative 26; Mismatches 70; Indels 322; Gaps 16;

OY 6 GTGYNNGYFY--YWN-----DG- 21
| | | | |
Db 414 GLDYNNXYLLSIEGDYWNKIDIEFKTGSKGIVLDNSGSKLNLVYHDIGEFAIHLRDS 473
OY 22 -----HGVYTYTG--PG-----32
| | | | |
Db 474 SNNSIDGCTIYNTGRTKPGEGGLYVSGDKGQHDYERACNNNTIENCTVGPVNTAEGVD 533
OY 33 -----GQFSVWMSNSGNFVG-----47
| | | | |
Db 534 VKEGTMTTIRNCVFSAEGISGENSSDAFIDLKGAAGFYVNTFNVDGSEVINTGVDFLD 593
OY 48 -GKMGPGTKNKVYNFSGSYN-----67
| | | | |
Db 594 RGTGFNTGFRNAL--FENTYNLGSRASEISTARKKQSPROTHWMDIRPNNSVDPISD 651
OY 68 -----PNCN-----SYLSVYGSNRNPLEIYIVNF-----93
| | | | |
Db 652 GTENLVNKKFCPDWNIIEPCNPVDETNQAPTISFLS-----PVNNITLVGYNLQVEVNA 704
OY 94 -----GTYNSTGATKLGCV 108
| | | | |
Db 705 TDADGTIDNVKLYIDNNLVQIINSTYKMGHSDSPNTDELNGLTEGYTLKALAT-----759
OY 109 TSDGSV-----YDIYRTQRYNQ-----PSITGTA 132
| | | | |
Db 760 DNDGASTETQFTLVITEQSPSENCDEPTPSGTLEDFDIKFSNVFELSGGSLSNLK 819
OY 133 TTYQYMSVRRNHSSGSGSVNTANHFMAAOGGLTGLTMDYQI---VAVEGFSSGSASITV 189
| | | | |
Db 820 TFTINMSQYNGLYQFSINTNN-----GVPDYIYNLKPKITFOFKNANPEISI 867
OY 190 S 190
Db 868 S 868

RESULT 28
US-10-093-037-63
: Sequence 63, Application US/10093037
: Publication No. US20030078397A1
: GENERAL INFORMATION:
: APPLICANT: Jay M. Short
: APPLICANT: Bylina, Edward
: APPLICANT: Swanson, Ronald V.
: APPLICANT: Mathur, Eric J.
: APPLICANT: Lam, David E.
: FILE REFERENCE: ENZYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS OF USE THEREOF
: FILE REFERENCE: 09010-024006
: CURRENT APPLICATION NUMBER: US/10/093,037
: CURRENT FILING DATE: 2002-03-06
: PRIOR APPLICATION NUMBER: US 09/910,579
: PRIOR FILING DATE: 2001-07-20
: PRIOR APPLICATION NUMBER: US 09/134,078
: PRIOR FILING DATE: 1998-08-13
: PRIOR APPLICATION NUMBER: US 08/949,026
: PRIOR FILING DATE: 1997-10-10
: PRIOR APPLICATION NUMBER: US 60/056,916
: PRIOR FILING DATE: 1996-12-06
: NUMBER OF SEQ ID NOS: 72
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 63
: LENGTH: 956
: TYPE: PRT
: ORGANISM: Bankia gouldi
US-10-093-037-63

Query Match 12.9%: Score 134.8; DB 9; Length 956;
Best Local Similarity 13.18; Pred. No. 2.4e+02;
Matches 63; Conservative 26; Mismatches 70; Indels 322; Gaps 16;
OY 6 GTGYNNGYFY--YWN-----DG- 21
| | | | |
Db 50 -----GW-----51

Db 414 GLDYNNXYLLSIEGDYWNKIDIEFKTGSKGIVLDNSGSKLNLVYHDIGEFAIHLRDS 473
OY 22 -----HGVYTYTG--PG-----32
| | | | |
Db 474 SNNSIDGCTIYNTGRTKPGEGGLYVSGDKGQHDYERACNNNTIENCTVGPVNTAEGVD 533
OY 33 -----GQFSVWMSNSGNFVG-----47
| | | | |
Db 534 VKEGTMTTIRNCVFSAEGISGENSSDAFIDLKGAAGFYVNTFNVDGSEVINTGVDFLD 593
OY 48 -GKMGPGTKNKVYNFSGSYN-----67
| | | | |
Db 594 RGTGFNTGFRNAL--FENTYNLGSRASEISTARKKQSPROTHWMDIRPNNSVDPISD 651
OY 68 -----PNCN-----SYLSVYGSNRNPLEIYIVNF-----93
| | | | |
Db 652 GTENLVNKKFCPDWNIIEPCNPVDETNQAPTISFLS-----PVNNITLVGYNLQVEVNA 704
OY 94 -----GTYNSTGATKLGCV 108
| | | | |
Db 705 TDADGTIDNVKLYIDNNLVQIINSTYKMGHSDSPNTDELNGLTEGYTLKALAT-----759
OY 109 TSDGSV-----YDIYRTQRYNQ-----PSITGTA 132
| | | | |
Db 760 DNDGASTETQFTLVITEQSPSENCDEPTPSGTLEDFDIKFSNVFELSGGSLSNLK 819
OY 133 TTYQYMSVRRNHSSGSGSVNTANHFMAAOGGLTGLTMDYQI---VAVEGFSSGSASITV 189
| | | | |
Db 820 TFTINMSQYNGLYQFSINTNN-----GVPDYIYNLKPKITFOFKNANPEISI 867
OY 190 S 190
Db 868 S 868

RESULT 29
US-09-995-749A-2
: Sequence 2, Application US/09995749A
: Patent No. US20020155568A1
: GENERAL INFORMATION:
: APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
: APPLICANT: DIJKHUIZEN, LUBBERT
: APPLICANT: RAHAOUI, HAKIM
: APPLICANT: LEER, ROBERT-JAN
: TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
: FILE REFERENCE: B043388-CIP
: CURRENT APPLICATION NUMBER: US/09/995,749A
: CURRENT FILING DATE: 2001-11-29
: PRIOR APPLICATION NUMBER: 09/604,957
: PRIOR FILING DATE: 2000-06-28
: PRIOR APPLICATION NUMBER: EPO 00201871.1
: PRIOR FILING DATE: 2000-05-25
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 1781
: TYPE: PRT
: ORGANISM: Lactobacillus reuteri
US-09-995-749A-2

Query Match 12.8%: Score 133.6; DB 9; Length 1781;
Best Local Similarity 14.28; Pred. No. 7.4e+02;
Matches 80; Conservative 20; Mismatches 80; Indels 384; Gaps 22;
OY 4 QPCTGYNNGYFY-----SYWNDGHGVTV-----TNGP-----G 32
| | | | |
Db 235 OPTFDKNNYAYLDTFEVRKNGELHATGMATNSAINVNHFFVILFDOTNCKEVARQREVE 294
OY 33 GQ-----FSY-----NNSNSGNFVGGK-----49
| | | | |
Db 295 GQSRPDYAKVYPVYGAANSFNVTFNISLDYTHQYVLSRYSNSDNGGDVNTYWFNP 354
OY 50 -----GW-----51

Db 355 QSIAPANOSGNYLDSFDSISKNGEYVYTGMMNATDLSLQNNHYVLLFDDTAGKQYASAKA 414
OY 52 -----OPGKMKYIN-FSGSYNPNGN----- 71
Db 415 DLISRPVAKAYPYKATATNGSEKYTEFVNNLQPOHOSVVSFRSADENGNDKRRHTDY 474
OY 72 -----SYLSVYGM-----SRNPLIEYIYVENG-----T 95
Db 475 WFSPIYLNQATSNIDITMTNGLHIGWMASSDINSINTTPYAIILNNGKEVTQKMSLT 534
OY 96 YNPSTGAT-----KL-----GEVTSDSGYD 116
Db 535 ARPVAAYAPPLYSNVAVSFGDTTIKLTNDYOALNGOLOVLLRFSKADGAPSGDNTVTD 594
OY 117 IY-----RTQRYNPS 127
Db 595 QFSKNYATTCGNFEDYKYNQVEFSGMHATNOSNDKDSOMIYLVNGKEVKROLVNDTK 654
OY 128 IIGTATFYQWYSVRN-----HRSGSYNT 152
Db 655 -EGAAGF-----NRNDYKYNPAIENSSMSGFOGIITLPYTKNENYQLVHFRSNDYKT 707
OY 153 --AAHFNAKA-----QOGL-TLCTNDYOIVANEG----- 178
Db 708 GEGNYVDWSELMPVKDSFOKNGPLAQOGLQTINGOQYIDPTTGPRKNFLLQSGNNW 767
OY 179 -YFSSGS-----ASITVS 190
Db 768 IYFSDPTGCVTNALLOLQFAKCTVS 791

RESULT 30

US-09-888-224-2

Sequence 2, Application US/09888224

Patent No. US20020120118A1

GENERAL INFORMATION:

APPLICANT: Lam, D. et al.

TITLE OF INVENTION: Endoglucanases

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/888,224

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/430,669

FILING DATE: 28-Oct-1999

APPLICATION NUMBER: US/08/651,572

FILING DATE: 22-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Charles J. Herron

REGISTRATION NUMBER: 28,019

REFERENCE/DOCKET NUMBER: 331400-48

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS: Unknown

TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-888-224-2

Query Match 12.7%; Score 133; DB 10; Length 553;
Best Local Similarity 11.8%; Pred. No. 1.2e+02;
Matches 58; Conservative 25; Mismatches 60; Indels 350; Gaps 18;

OY 1 OTIDPGT----- 7
Db 59 QSVKPTWPTPAIDYAKNPDLQGLDSVOIMEKIIKAGDLGIFLLDYHRIGCNFIEPLWY 118
OY 8 -----GYNGY-----FYSYV-----NDHGCG-----YTNNGPG-----GQFSV 37
Db 119 TDSFSEDYINTWVEVNAQRFCKYNNVIGADLKNRPHSSPAPAAVYTGSGATWGMGNAT 178
OY 38 NMSNSGN-----FY-----GKGWQPGT----- 55
Db 179 DWNLAERIGRAILEVAPQWVIFVEGQFTTPEIDGRYKMGHNMGMGNLGVKRYPNL 238
OY 56 -KNRVI-----NSYLSVYGMARNPLIEYIYVENFG-----NFGSY 66
Db 239 PRDKVVISPOYVGSSEYIDQPFDPGEGFPDNLPEIMWHHGYVLDLGYPVIGEFGRY 298
OY 67 NPNG-----NSYLSVYGMARNPLIEYIYVENFG----- 94
Db 299 GHGDDPRDVTWQNKIIDMWMQKFCDFPYSWMN-----NSGDRGGLKDDWTTIME 350
OY 95 -----TYNST----- 100
Db 351 DKYNNLRKLMDSGSGNATAPSPRTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 410
OY 101 -----GATKIGEYVSDG 112
Db 411 TTTTPSNNVPEEIVNVLTSSQYEGTSVEYVCDGTQCASSWYKAPNLMGVYKIGNATMDP 470
OY 113 SVY---DIYRTQRYNQPSIICTATFYQWYSVRNRHSSGSYNTANHFN----- 157
Db 471 NVCMGDEVYKT---AQDIDGTG---STKMEIR-NGVLKYNLNMNIMHPRKYNMAY 519
OY 158 -----ANAOQ 162
Db 520 PEVIYGAKPWGNQ 532

RESULT 31

US-09-797-464A-4

Sequence 4, Application US/09797464A

Publication No. US20030022807A1

GENERAL INFORMATION:

APPLICANT: Willeing, Reinhard

APPLICANT: Bjornvad, Mads Eskelund

APPLICANT: Kauppinen, Markus Sakari

APPLICANT: Schultein, Martin

TITLE OF INVENTION: Family 5 xyloglucanases

FILE REFERENCE: 6073.200-US

CURRENT APPLICATION NUMBER: US/09/797,464A

FILING DATE: 2002-02-19

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 400

TYPE: PRT

ORGANISM: Paenibacillus sp.

US-09-797-464A-4

Query Match 12.7%; Score 132.9; DB 9; Length 400;
Best Local Similarity 18.8%; Pred. No. 73;
Matches 68; Conservative 23; Mismatches 50; Indels 221; Gaps 22;
OY 6 GTGYNNG-----YF----- 14
Db 48 GAGWNLGNQLEATVNGVSEFAMGNPVVTPDLIKKYKAGFKTIRIPVSYLNHIGAPNY 107


```
Db 179 KTELHVSEFOEGSKLIMEPGAVLSNONIANGALAINGLITLIDSSMGTPOAGEIFSPPE 238
|:|
QY 63 -----SGS-----YNPNG 70
Db 239 LKIVATTSASGSGSVSSIPNPKRISAAPVSGSAATPTMSENKVELTGLDITLIDPNG 298
|:|
QY 71 NSYLSVYGSRNPLIEYIVENFGYNPSTGA-----TKLGEVTSDGSVYDI-----117
|:|
Db 299 NRY-----ONPMLGSDLDVPLKLPNTNSDVQYVDLTLSGDLF 336
|:|
QY 118 ----YRTQRYNOPSIIGTATF-----YQWVSV--RRNHRSSGSV-----150
|:|
Db 337 POKGY-----MGTTLDSNPQTKLQARMTFDTYRRWYIIPRDNHFYANSILGSQ 386
|:|
QY 151 -----NTAN-----HFNAN-----AOGGLTL-----GTMDOYI 173
|:|
Db 387 NSMIVYKGLINMLNNAFDDIATNMFVSGVGTFLAQQGTPPLSEEFYSYRGTS-----442
|:|
QY 174 VAVE-----GYFSSGS-----ASI 187
|:|
Db 443 VALDAKPRQDFILGAFAFSKIVCKTKAIKKMHNFFHKSEYSYQASV 488
|:|
```

```
RESULT 36
US-10-090-624-4
: Sequence 4, Application US/10090624
: Patent No. US20020132335A1
: GENERAL INFORMATION:
: APPLICANT: TAKAKURA, Hikaru
: APPLICANT: MORISHITA, Mio
: APPLICANT: SHIMOJO, Tomoko
: APPLICANT: ASADA, Kiyozo
: APPLICANT: KATO, Ikunoshin
: TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
: FILE REFERENCE: TAKAKURA-6
: CURRENT APPLICATION NUMBER: US/10/090,624
: PRIOR FILING DATE: 2002-03-06
: PRIOR APPLICATION NUMBER: 09/445,472
: PRIOR FILING DATE: 1999-12-06
: PRIOR APPLICATION NUMBER: 151969/1997
: PRIOR FILING DATE: 1997-06-10
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 4
: LENGTH: 522
: TYPE: prt
: ORGANISM: Pyrococcus furiosus
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (428)..(428)
: OTHER INFORMATION: xaa at position 428 is Gly or Val.
US-10-090-624-4
```

```
Query Match 12.6%; Score 131.8; DB 12; Length 522;
Best Local Similarity 13.5%; Pred. No. 1.3e+02;
Matches 65; Conservative 19; Mismatches 46; Indels 352; Gaps 19;
```

```
QY 8 GYN-----NCFYSYNNNDGHCYTY-----27
|:|
Db 22 GYDGSITIGIIDTGDASHPDLQCKVIGWDFVNGRSYPYDDHGHG--THVASIAGTG 79
|:|
QY 28 --TNG-----PGGQFS-----VNMS-----40
|:|
Db 80 AASNGKYKGMAPGAKLAGIKVLGADSGSISITLIKVEWAVDNKKYGIKVINLSLGSQ 139
|:|
QY 41 -----NSG-----43
|:|
Db 140 SSDGTDLALSOAVNAAMDAGLVVVAAGNSGPNKYYTIGSPAASKVITVGAVDKYDVTSF 199
|:|
QY 44 -----NFGCKGW-----QPGTK-----56
|:|
Db 200 SSRGPTADGRLEPEYVAPGNMTIIAARASGTSMGOPINDYYTAAPGTSMTPHVAGIALLL 259
|:|
```

```
QY 57 -----NKNVNF-----62
|:|
Db 260 LOAHPSWTPDKVKTALLETADIYKPEIDIAVYAGARVNAVKAINDNAKLVTGYVAN 319
|:|
QY 63 -----SGS-----YNPNG-----SYLSVYGSRNPLIEY 88
|:|
Db 320 KCSQTHQFVIGSASFEVATLTYMDNANSDLDLXYLPNGNQVDYVSTAYYGF-----370
|:|
QY 89 IYENFGTYNPSG-----ATKLGEVTSDGSVYDIKRTQRYNOPS-----11GT 131
|:|
Db 371 --EKVGYNPTDGTWTIKVYSVGSANYQVDVSDGSL-----SQGSSPSQPEPTVDA 423
|:|
QY 132 ATF-----YQWVSVRNHRSSGSVNTANFNMAAQGLITGMDYQIVAVEGYFSSGSAS 186
|:|
Db 424 KTFQXSDHYIY-----DKSDIFTYTVN-----SGATK 450
|:|
QY 187 IT 188
|:|
Db 451 IT 452
|:|
```

```
RESULT 37
US-10-090-624-16
: Sequence 16, Application US/10090624
: Patent No. US20020132335A1
: GENERAL INFORMATION:
: APPLICANT: TAKAKURA, Hikaru
: APPLICANT: MORISHITA, Mio
: APPLICANT: SHIMOJO, Tomoko
: APPLICANT: ASADA, Kiyozo
: APPLICANT: KATO, Ikunoshin
: TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
: FILE REFERENCE: TAKAKURA-6
: CURRENT APPLICATION NUMBER: US/10/090,624
: PRIOR FILING DATE: 2002-03-06
: PRIOR APPLICATION NUMBER: 09/445,472
: PRIOR FILING DATE: 1999-12-06
: PRIOR APPLICATION NUMBER: 151969/1997
: PRIOR FILING DATE: 1997-06-10
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 16
: LENGTH: 654
: TYPE: prt
: ORGANISM: Pyrococcus furiosus
US-10-090-624-16
```

```
Query Match 12.6%; Score 131.8; DB 12; Length 654;
Best Local Similarity 13.5%; Pred. No. 1.8e+02;
Matches 65; Conservative 19; Mismatches 46; Indels 352; Gaps 19;
```

```
QY 8 GYN-----NCFYSYNNNDGHCYTY-----27
|:|
Db 154 GYDGSITIGIIDTGDASHPDLQCKVIGWDFVNGRSYPYDDHGHG--THVASIAGTG 211
|:|
QY 28 --TNG-----PGGQFS-----VNMS-----40
|:|
Db 212 AASNGKYKGMAPGAKLAGIKVLGADSGSISITLIKVEWAVDNKKYGIKVINLSLGSQ 271
|:|
QY 41 -----NSG-----43
|:|
Db 272 SSDGTDLALSOAVNAAMDAGLVVVAAGNSGPNKYYTIGSPAASKVITVGAVDKYDVTSF 331
|:|
QY 44 -----NEVGCKGW-----QPGTK-----56
|:|
Db 332 SSRGPTADGRLEPEYVAPGNMTIIAARASGTSMGOPINDYYTAAPGTSMTPHVAGIALLL 391
|:|
QY 57 -----NKNVNF-----62
|:|
Db 392 LOAHPSWTPDKVKTALLETADIYKPEIDIAVYAGARVNAVKAINDNAKLVTGYVAN 451
|:|
QY 63 -----SGS-----YNPNG-----SYLSVYGSRNPLIEY 88
|:|
```

```
Db 452 KGSQTHQVYSGASFVATLTYMDNANSDDLTYLDENGNQVDYSTYAYVGF----- 502
QY 89 IVENFGTYPSTG-----ATKLGCVTSDGSVDYRTQVKNOPS-----IIGT 131
Db 503 ---EKVGYVNTDGTMTIKVYVSGSANYOVVDVSDSL-----SOPGSSPSQPEPTVDA 555
QY 132 ATF-----YQVMSVRNRHSSGSVNTANHFNAMAQOGLTGTMDYQIVAVEGYFSSGSAS 186
Db 556 KTFQSGDHYT-----DSSDFTMTVY-----SGATK 582
QY 187 IT 188
Db 583 IT 584

RESULT 38
US-09-815-242-4989
: Sequence 4989, Application US/09815242
: Patent No. US20020061569A1
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Karl L.
: APPLICANT: Zyskind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: FILE REFERENCE: ELITRA.011A
: CURRENT APPLICATION NUMBER: US/09/815,242
: CURRENT FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4989
: LENGTH: 742
: TYPE: PRF
: ORGANISM: Enterococcus faecalis
US-09-815-242-4989

Query Match 12.6%; Score 131.2; DB 10; Length 742;
Best Local Similarity 13.7%; Pred. No. 2.4e+02;
Matches 65; Conservative 28; Mismatches 64; Indels 318; Gaps 19;

QY 7 TGYNNGYFS-----YWDG---HGGVY---TNG--- 30
Db 105 TCQNNKLYAEKKDFDDIAELAKYTKLDKKTALKYLNNGIHEDSGSTOYQVEFGTGGONI 164
QY 31 -----PGGFS---VNMSNSGN-----FYGGG 50
Db 165 TLETROKIEADLKKKKISGVYFNEHPARLYPNGQFASHFIGYTKANPDDEKGLVGANG 224
QY 51 ----- 50
Db 225 LEOYNDILSGTDGRVYFEKOIYGNALPSTVAEKKAVDGGDIYTTLDLRLONTLEDLMT 284
QY 51 -----WQ-----PGTK 56
```

```
Db 285 QVNEKYEPMYAMLMKAEKTGEIVAMSQRPTENPETKQGLDNGTQNLVESPYPGSGT 344
QY 57 NKVYNS-----GSYP-----NGNSYLS---VYGSRN- 82
Db 345 IKLETTAASMEQOQFNPENLFNVEGCIQVGDVYVNDHDYTRLNKGEYLVROAISWSSNI 404
QY 83 -----PLIEYIVENGTGYNPSTGATKIGE----- 107
Db 405 GMYKLEQKNKDEKWMYELKKFGFGT---STHSLGSESGKLPCTNFVDRAMSATGQAIT 461
QY 108 -----VTSQSVYDIYRTOR-----VNQPSLIGTATFYQVMSVRNRH 145
Db 462 VTFNQMKGFSAIANGDSMLQPHYISKYVDKNTGKETITEPQIVGTPIKAQ----- 512
QY 146 SSGSVNTANHFNAMAQOGLT--LGTMD-----YQIVAVEGYF---SSGSASIT 188
Db 513 -----TAQQIRTYMIDTVEDPTGYIAYDVRVPGYHAAKTGTAQIS 554

RESULT 39
US-09-815-242-10634
: Sequence 10634, Application US/09815242
: Patent No. US20020061569A1
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Karl L.
: APPLICANT: Zyskind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: FILE REFERENCE: ELITRA.011A
: CURRENT APPLICATION NUMBER: US/09/815,242
: CURRENT FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10634
: LENGTH: 742
: TYPE: PRF
: ORGANISM: Enterococcus faecalis
US-09-815-242-10634

Query Match 12.6%; Score 131.2; DB 10; Length 742;
Best Local Similarity 13.7%; Pred. No. 2.4e+02;
Matches 65; Conservative 28; Mismatches 64; Indels 318; Gaps 19;

QY 7 TGYNNGYFS-----YWDG---HGGVY---TNG--- 30
Db 105 TCQNNKLYAEKKDFDDIAELAKYTKLDKKTALKYLNNGIHEDSGSTOYQVEFGTGGONI 164
QY 31 -----PGGFS---VNMSNSGN-----FYGGG 50
Db 165 TLETROKIEADLKKKKISGVYFNEHPARLYPNGQFASHFIGYTKANPDDEKGLVGANG 224
QY 51 ----- 50
```

Db 225 LEQTYNDILSGTGRVFEKDIYGNALPGTVAEKKAVGODIYTTLLDSRLONTLEDLMT 284
QY 51 -----WQ-----PGMK 56
Db 285 OVNEXEYEVSMTAMLEAKTGEIVAMSORPTFPNETKOGCLDNGWMLVESPPEPST 344
QY 57 NKVINFSGSYNP-----NGNSYLS--VYGMSRN- 82
Db 345 IKLFPTAASMEGCGPNPELFRNVRGIVQGVYVNDHYTRLNGKEVLYNRAISMSSNI 404
QY 83 -----PLEYIIVENFGTYNPSTGATKIGE----- 107
Db 405 GMVKLEOKMGDEKMEYKKEFGFT--STHSGLSGESAGKLPGTNFVDRAMSAFGAIT 461
QY 108 -----VTSDSGVYDIYRTQR-----VNPSIICTATFYQWYSRRHR 145
Db 462 VTNFQMKGFSAIANDGSMLOPHYSIKYVDKNKTETITEPOTVGTPIKAQ----- 512
QY 146 SSGSVNTANHFMAAQQGLT--LGTM-----YQIVAVEGYF--SSGSASIT 188
Db 513 -----TMOQIRTYMIDIVEDPTGYIAVDIKVPGYHVAAKTGTQAOIS 554

RESULT 40
US-09-782-906-2
; Sequence 2, Application US/09782906
; Patent No. US20010051369A1
; GENERAL INFORMATION:
; APPLICANT: Delagrave, Simon
; APPLICANT: Rittenhouse Pruss, Jennifer L.
; APPLICANT: Murphy, Dennis J.
; APPLICANT: Maffia III, Anthony M.
; APPLICANT: Bylina, Edward J.
; APPLICANT: Coleman, William J.
; TITLE OF INVENTION: Variant Galactose Oxidase, Nucleic Acid Encoding Same, And Method
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: HER-0040
; CURRENT APPLICATION NUMBER: US/09/782,906
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/185,001
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Dactylium dendroides
US-09-782-906-2

Query Match 12.5%; Score 130.9; DB 10; Length 639;
Best Local Similarity 13.8%; Pred. No. 1.9e+02;
Matches 68; Conservative 34; Mismatches 68; Indels 321; Gaps 23;
QY 4 OPGTGY-----NNG---YFYSYNDGHGCVTYTNGPGG-QFSVMSN 41
Db 155 OPGICRMGPTTIDLPVPAAAAEPTSGRYLWMSYRNDAFGG-----SPGCITLTSSMDP 209
QY 42 SGNFY-----GSK-----GMQPG----- 54
Db 210 STGIYSDRTYVYTKHDMFCPGISMDNGQIVYTGNDAAKKTSLYDSSSDSWIPGDMQYA 269
QY 55 -----TNKKNVINFSGS-----YFNNGNSYLS----- 75
Db 270 RGYOSSATMSDGRVFTTIGSSWGSVGEFEKNGEYFSSKWTWISLPNAKVNPMULTADKQGLY 329
QY 76 -----YVGSRNPLIE-----YYI----- 89
Db 330 RSDNHAMLFQMKKGSVFPAGPSTAMNMYTTSGSGDVKSAGKROSNRGVAPDAMCGNAVY 389
QY 90 -----VENFG--TYNPSTGATK-----LGE-----VTSQ 111
Db 390 DAVKGIILTFGSGSPDYQSDATTNAHITTLGEPGTSPTVTFASNGLYFARTFHTSVVLPD 449

QY 112 GSVY-----DIYRTORVNPSSIIGTATFYQ-----YMSVR- 141
Db 450 GSTFITGQORGIPEPREDSTPVFTPEIYVPEQ-----DTFYQONNSIVRYVHISL 500
QY 142 -----RNRHSSGSV--NTANHFNA-----WAOGLTLG--- 167
Db 501 LLPDGRVENGGGGLCGDCTTNHFDQAIFTPNYLYNSNGNLATRPKITRPTSTQSVKVGRI 560
QY 168 -----IMDYOI-----YAVEGYF-- 180
Db 561 TTSDDSSISKASLIRYGTATHTVNTDORRIPLLTLTNGNSYSFQVPSDSGVALLPGYML 620
QY 181 -----SSGSASI 187
Db 621 FVMNAGVPSV 631

RESULT 41
US-09-782-906-3
; Sequence 3, Application US/09782906
; Patent No. US20010051369A1
; GENERAL INFORMATION:
; APPLICANT: Delagrave, Simon
; APPLICANT: Rittenhouse Pruss, Jennifer L.
; APPLICANT: Murphy, Dennis J.
; APPLICANT: Maffia III, Anthony M.
; APPLICANT: Bylina, Edward J.
; APPLICANT: Coleman, William J.
; TITLE OF INVENTION: Variant Galactose Oxidase, Nucleic Acid Encoding Same, And Met
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: HER-0040
; CURRENT APPLICATION NUMBER: US/09/782,906
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/185,001
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NO. US20010051369A1el sequence
US-09-782-906-3

Query Match 12.5%; Score 130.9; DB 10; Length 639;
Best Local Similarity 13.8%; Pred. No. 1.9e+02;
Matches 68; Conservative 34; Mismatches 68; Indels 321; Gaps 23;
QY 4 OPGTGY-----NNG---YFYSYNDGHGCVTYTNGPGG-QFSVMSN 41
Db 155 OPGICRMGPTTIDLPVPAAAAEPTSGRYLWMSYRNDAFGG-----SPGCITLTSSMDP 209
QY 42 SGNFY-----GSK-----GMQPG----- 54
Db 210 STGIYSDRTYVYTKHDMFCPGISMDNGQIVYTGNDAAKKTSLYDSSSDSWIPGDMQYA 269
QY 55 -----TNKKNVINFSGS-----YFNNGNSYLS----- 75
Db 270 RGYOSSATMSDGRVFTTIGSSWGSVGEFEKNGEYFSSKWTWISLPNAKVNPMULTADKQGLY 329
QY 76 -----YVGSRNPLIE-----YYI----- 89
Db 330 RSDNHAMLFQMKKGSVFPAGPSTAMNMYTTSGSGDVKSAGKROSNRGVAPDAMCGNAVY 389
QY 90 -----VENFG--TYNPSTGATK-----LGE-----VTSQ 111
Db 390 DAVKGIILTFGSGSPDYQSDATTNAHITTLGEPGTSPTVTFASNGLYFARTFHTSVVLPD 449
QY 112 GSVY-----DIYRTORVNPSSIIGTATFYQ-----YMSVR- 141
Db 450 GSTFITGQORGIPEPREDSTPVFTPEIYVPEQ-----DTFYKONNSIVRAYHISL 500

QY 142 -----RNHRSSGSV---NTANHFNA-----WAQGLTLG--- 167
| | | | |
Db 501 LLPDGRVFNFGGGLCGDCTTNHFDQIIFTPNLYNSNGNLATRPKTRTSTOSYKVGGR 560
QY 168 -----TMDYOI-----VAEGYF--- 180
| | | | |
Db 561 T1STDSSISKASLIRYGTATHTVNTDORRIPLTLTNNGNSYSFQVPSDGVALLPGYWML 620
QY 181 ----SSGSASI 187
| | | | |
Db 621 FWMNSAGVPSV 631

RESULT 42
US-09-782-906-4
Sequence 4, Application US/09782906
Patent No. US20010051369A1
GENERAL INFORMATION:
APPLICANT: Delagrave, Simon
APPLICANT: Rittenhouse Pruss, Jennifer L.
APPLICANT: Murphy, Dennis J.
APPLICANT: Maffia III, Anthony M.
APPLICANT: Bylina, Edward J.
TITLE OF INVENTION: Variant Galactose Oxidase, Nucleic Acid Encoding Same, And Method
FILE REFERENCE: HER-0040
CURRENT APPLICATION NUMBER: US/09/782,906
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/185,001
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 639
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: No. US20010051369A1el Sequence
US-09-782-906-4

Query Match 12.5%; Score 130.9; DB 10; Length 639;
Best Local Similarity 13.6%; Pred. No. 1.9e+02;
Matches 67; Conservative 33; Mismatches 70; Indels 321; Gaps 21;

QY 4 QPCTG-----YNNGF-----YSTWN----- 19
| | | | |
Db 155 QPGLGHWGPTIDLPYPAAAIEPTSGRVLWMSSTRNDAFAGSPGIFLTLSSWDPSTGIV 214
QY 20 -----DGHGCVTYTNG-----PGGQF 35
| | | | |
Db 215 SDRTVYTKHDMFCPGISMDNGQIVVTGNDAAKTSLYDSSSDSWIPGDMQVANGYOS 274
QY 36 SVNMSNSGNFVGKGNQPGT--KNKYINFGSYNPNNGSYLS----- 75
| | | | |
Db 275 SATMSDGRVFTIGSGWSGVFEKNGEV-----YSPSKTWTSLPNKAVNPMLTADKGLY 329
QY 76 -----YVGNRNPLIE-----YYI----- 89
| | | | |
Db 330 RSDNHAMLEFGMKGSYFQAGPSTAMNMYTSGSGDVKSAGKROSNRGVAPDAMSGNAVY 389
QY 90 -----VENFG---TYNPSTGATK-----LGE-----VTSQ 111
| | | | |
Db 390 DAVKCKILTFGGSPPYODSDATTNHIIITLGEPTGSPNTVFASNGLHFAFTHTSVVLPD 449
QY 112 GSVY-----DIYRQARNQPSIICTATFYQ-----YWSVR- 141
| | | | |
Db 450 GSTFTTCGGRGCIPEEDSTPVFTPEIYVDEQ-----DFEYKONPNSIVRAVHSISL 500
QY 142 -----RNHRSSGSV---NTANHFNA-----WAQGLTLG--- 167
| | | | |
Db 501 LLPDGRVFNFGGGLCGDCTTNHFDQIIFTPNLYNSNGNLATRPKTRTSTOSYKVGGR 560

QY 168 -----TMDYOI-----VAEGYF--- 180
| | | | |
Db 561 T1STDSSISKASLIRYGTATHTVNTDORRIPLTLTNNGNSYSFQVPSDGVALLPGYWML 620
QY 181 ----SSGSASI 187
| | | | |
Db 621 FWMNSAGVPSV 631

RESULT 43
US-09-782-906-5
Sequence 5, Application US/09782906
Patent No. US20010051369A1
GENERAL INFORMATION:
APPLICANT: Delagrave, Simon
APPLICANT: Rittenhouse Pruss, Jennifer L.
APPLICANT: Murphy, Dennis J.
APPLICANT: Maffia III, Anthony M.
APPLICANT: Bylina, Edward J.
TITLE OF INVENTION: Variant Galactose Oxidase, Nucleic Acid Encoding Same, And Met
FILE REFERENCE: HER-0040
CURRENT APPLICATION NUMBER: US/09/782,906
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/185,001
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 639
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: No. US20010051369A1el Sequence
US-09-782-906-5

Query Match 12.5%; Score 130.9; DB 10; Length 639;
Best Local Similarity 13.8%; Pred. No. 1.9e+02;
Matches 68; Conservative 34; Mismatches 68; Indels 321; Gaps 23;

QY 4 QPCTG-----NNG---YFYSYWNDCGCVTYTNGCGG--QFSYNSN 41
| | | | |
Db 155 QPGLGHWGPTIDLPYPAAAIEPTSGRVLWMSSTRNDAFGG-----SPGGLTLTLSSWDP 209
QY 42 SCGFV-----GCK-----GWQPG----- 54
| | | | |
Db 210 STGIVSDRTVYTKHDMFCPGISMDNGQIVVTGNDAAKTSLYDSSSDSWIPGDMQVA 269
QY 55 -----TKNKVINFGS-----YNPNGNSYLS----- 75
| | | | |
Db 270 RGYSSATMSDGRVFTIGSGWSGVFEKNGEVYSPSKTWTSLPNKAVNPMLTADKGLY 329
QY 76 -----YVGNRNPLIE-----YYI----- 89
| | | | |
Db 330 RSDNHAMLEFGMKGSYFQAGPSSAMNMYTSGSGDVRSAGKROSNRGVAPDAMSGNAVY 389
QY 90 -----VENFG---TYNPSTGATK-----LGE-----VTSQ 111
| | | | |
Db 390 DAVKCKILTFGGSPPYODSDATTNHIIITLGEPTGSPNTVFASNGLHFAFTHTSVVLPD 449
QY 112 GSVY-----DIYRQARNQPSIICTATFYQ-----YWSVR- 141
| | | | |
Db 450 GSTFTTCGGRGCIPEEDSTPVFTPEIYVDEQ-----DFEYKONPNSIVRAVHSISL 500
QY 142 -----RNHRSSGSV---NTANHFNA-----WAQGLTLG--- 167
| | | | |
Db 501 LLPDGRVFNFGGGLCGDCTTNHFDQIIFTPNLYNSNGNLATRPKTRTSTOSYKVGGR 560
QY 168 -----TMDYOI-----VAEGYF--- 180
| | | | |
Db 561 T1STDSSISKASLIRYGTATHTVNTDORRIPLTLTNNGNSYSFQVPSDGVALLPGYWML 620

OY 181 ----SSGSASI 187
Db 621 FVMNSAGVPSV 631

RESULT 44
US-09-741-669-304
Sequence 304, Application US/09741669
Patent No. US20020022718A1
GENERAL INFORMATION:
APPLICANT: Forsyth, R. Allyn
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for
FILE REFERENCE: ELITRA 009A
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 304
LENGTH: 1325
TYPE: PRF
ORGANISM: Escherichia coli
US-09-741-669-304

Query Match 12.5%; Score 130.8; DB 10; Length 1325;
Best Local Similarity 13.5%; Pred. No. 6.3e+02;
Matches 70; Conservative 27; Mismatches 68; Indels 352; Gaps 21;

OY 2 TIOPG-----TGYN-----NGVF----- 14
Db 255 TIREGLVTAENTIIIGGNATIGITLVQDQSVITVRRLYNGIFGNGIVNISNGLINK 314
OY 15 -YS-----YWN----- 19
Db 315 EYSLVGVQDQSHGVVNTDKGMHNLGCTGEAFRIYIIGDAGDELNVSSSEGVDSGITTA 374
OY 20 -----DHC-----GVYTTNG----- 30
Db 375 GKMETGTGNTIVKDKNSVITNLGTLNGYDGHGEMNISNOGLVYNSGSSSLGCGETGVNV 434
OY 31 ---PGGFSV-----NMSGNFV-----GGKMGSTKN----- 57
Db 435 SITTGGMVEVKNVYTTTIGVAGVGNLNIISDGKEVSQNTIFLGDKASGIGTLMDATSS 494
OY 58 -----KVINFSGSYNPNGNSYLSYG-----WS----- 80
Db 495 FDTVGINVGNFGSGIYNVNSNGATLNTSTGYGFIGNMSGKGINVISTDSLMLNLTSSSTNAQ 554
OY 81 -----RNPLEY----- 88
Db 555 LLQVGLTGTGELNITGGIVKARDQIALNDKSGDVRVQDQNSLLETFTMYVGTSGTGT 614
OY 89 -IVENGTNPSGTATKLEVTSDGSVDYIRQVRNPSI-----IGTA----- 132
Db 615 LLLTNNGLTNVEGGEVYLG-----VFPAVGLTNTGAHGEAADAAGT 658
OY 133 -----TFYQWVSVRNRHRSQS-----VNTANH--FN 157
Db 659 TNATKEVFLGEGVEF-----NHTNNSDAGYQVDMLTIGDDOKGVINDAGHTVFN 710
OY 158 AM-AOQGLT---GTMDYQIVAVEGFFSSGSASTVS 190
Db 711 AGNTYSGKTLVNDGLTITASHRADGVGTGMSSEVTIA 747

RESULT 45
US-09-924-097-14
Sequence 14, Application US/09924097

Patent No. US20020156240A1
GENERAL INFORMATION:
APPLICANT: TOMONO, Jun
APPLICANT: NOMURA, Yoshiko
APPLICANT: SAGAWA, Hiroaki
APPLICANT: SAKAI, Takeshi
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: ALPHA-AGARASE AND PROCESS FOR PRODUCING THE SAME
FILE REFERENCE: TOMONO-1
CURRENT APPLICATION NUMBER: US/09/924,097
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: JP00/00966
PRIOR FILING DATE: 2000-02-21
PRIOR APPLICATION NUMBER: 11-44890
PRIOR FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: 11-198852
PRIOR FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 925
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Amino acid sequence of agarase 1-7
US-09-924-097-14

Query Match 12.5%; Score 130.4; DB 9; Length 925;
Best Local Similarity 8.9%; Pred. No. 3.7e+02;
Matches 76; Conservative 29; Mismatches 67; Indels 686; Gaps 22;

OY 10 NNGEFS-----YWNDSHGVTYTNQ-----PGGFSVN----- 38
Db 39 NSCGTFADQANPITITYTNGCEQALSYVACGVYVDYINTEGGDYSVEVLNCTVAASGPT 98
OY 39 -----WSNSG-----NF-----VGKGMQ----- 52
Db 99 IEMLVKGVWVSQGVAVAPQGSMDNFPPLSPSHLTLPAQAASIRLHAIGSNMGNLES 158
OY 53 -----PG-----TKKVINFS----- 63
Db 159 FSLQVTPLEGASVADVVELENFINTDKDRNAIAGDSVYVGFTGNTNGINFTLGDYADY 218
OY 64 -----GSYNP-----NGNSYLSV-----GWS----- 80
Db 219 HVNFASPGTYNYSIAGSTVQOIGAEILLNCTVANSNTLSATAGDDYODFALTCGYLI 278
OY 81 ----- 80
Db 279 ANAGHTTIRKVSYSANMOMNGDSITFTHISDDTNGSNQAMHLEPPVAIPESRIKSS 338
OY 81 ----- 87
Db 339 WMYTPQNSNLACGSDPGATGAFWGHMPEEDLYDSGLSNMVNOGYRNGLDYVGRGE 398
OY 88 -----YIENFG-----TYP----- 98
Db 399 FDMGFPMFLIEYVGDPTSHARTLDDPILMSFNGHEHNGYLNGLMSNISPFTVDFKSO 458
OY 99 -----STGATKLEVTSDGSVY-----DIYRQVRNPSI----- 128
Db 459 VDALLSANVSHIMFDSQTSSTKSTDLGFGGDFSTWMDAFREYMRDKYTTAELNFKGIT 518
OY 129 ----- 128
Db 519 NINAENRYNRLSRGYTHASVMAANKITSGIPLFDDFIYFNRAVLNERMAEVLDIRSI 578
OY 129 ---IGTAT----- 133
Db 579 DADIEIGATTALTEANGYIFDKDLTFLAGELMAGSAVADDEMPITIIISHLSAEAVKTLV 638
OY 134 -----FYQ 136

Db 639 YFPYPMNFKDLDRNSDPQARTWIAOSYANGAIFSPANWYIGDAGVWSPGADNRYDLQ 698
137 Y-----W-----SVR-----141
Db 699 FASDNALLDGYAFKVGGLVSPMMSLDTTWIDGSRLOTSTRYLIENNLNFDLIFGD 758
142 -----141
Db 759 PGKPVPTQAQALDAIIVDSRKYLTDAQNLNLDANNQKVIDLNNADTAIINALKAT 818
142 -----RNHSSGS-----VNTAHFNMAAOGLTGTMDY 171
Db 819 NISVTIGNMAADDTTALSRYHESNNAPYIQLNRPVNPAN-----GYTPVLSNV 870
Qy 172 QIVAVEGFSSGSASITV 189
Db 871 KIAIPQCFEFCITQATV 888

RESULT 46
US-10-002-309B-2
Sequence 2, Application US/10002309B
Patent No. US20020160433A1
GENERAL INFORMATION:
APPLICANT: WISCONSIN ALUMNI RESEARCH FOUNDATION
TITLE OF INVENTION: E. COLI O157:H7 C1 ESTERASE INHIBITOR-BINDING PROTEIN AND METHODS
FILE REFERENCE: 096429-9117
CURRENT APPLICATION NUMBER: US/10/002.309B
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/243,675
PRIOR FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 886
TYPE: PRP
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: E. coli O157:H7 plasmid pO157
US-10-002-309B-2

Query Match 12.5% Score 130.3; DB 9; Length 886;
Best Local Similarity 12.1% Pred. No. 3.5e+02;
Matches 66; Conservative 31; Mismatches 72; Indels 377; Gaps 18;
Qy 1 QTI-----QPGTGYNNGYFYSWNDG-----21
Db 316 QTIPTVSRMIVNNYAPRLHLKLVMLPTGELLTMDPGNG-----WHSSTMORIGKEL 367
Qy 22 -----HGC-----VTYING 30
Db 368 VSHGIDNANYGLNSTAGLGENSHPRVYAQLAHNSRGNVANGIOVHGSGGCGIVTLDSF 427
Qy 31 PGCGFVSNNNS--GNFVCG-----KGWOPGTYKNKVINF-----62
Db 428 LGNEFSGHEVGHANGLGHVYDGFKGSVYRSAENNNSTWGMGDKRPIPNFYPSQTNKSC 487
Qy 63 -----SGS-----YNPNNGNSYLSV-----77
Db 488 LNNOCCEPRFGHFGFDAMAGSGSPSANAARFTWYTPSSAIIORFENKAVEDSRSGTGF 547
Qy 78 -----GMSRNPIL 85
Db 548 SKMNADTOEMEPYHTIDRAEQITASVNELESEKMAELMAEYAVVYVHMNGMWTNR---604
Qy 86 EYIIVENFGTYNPSTGATKICEV-----TSDGSYV 115
Db 605 -----IYIPTASADNRGSLITINHEAGYNSYLFINGDEKVVSGYKKSFFVSDGQFW 655
Qy 116 ---DIYRTORVNOPSLI-----GTAIFYQYWSV-----140
Db 656 KENDVYDTRKARKPEQFGVPTVTLVGYDPEGLSSYIYPAMYGAVGFTYSDDSQNLSDN 715

Qy 141 -----RNHSSGSVNTAHFN-----AWA 160
Db 716 DCQLOVDTKREGQLRFLANRANNTYNNKRHINPIESPOTATLVCKNKKILDTKSLTPA 775
Qy 161 OQGLTGTMDYQ-----YVAVEGFSSGS- 184
Db 776 PEGITY-TVNGQALPAKENEGCIYVNSGKRYCLPVGQBSGYSLPDMIVGQGEYVDSGAK 834
Qy 185 ASITVS 190
Db 835 AKVLLS 840

RESULT 47
US-09-797-464A-2
Sequence 2, Application US/09797464A
Publication No. US20030022807A1
GENERAL INFORMATION:
APPLICANT: Bjornvad, Mats Eskelund
APPLICANT: Bjornvad, Mats Eskelund
APPLICANT: Kauppinen, Markus Sakari
APPLICANT: Kauppinen, Markus Sakari
TITLE OF INVENTION: Family 5 xyloglucanases
FILE REFERENCE: 6073.200-US
CURRENT APPLICATION NUMBER: US/09/797,464A
CURRENT FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 395
TYPE: PRP
ORGANISM: Paenibacillus pabuli
US-09-797-464A-2

Query Match 12.4% Score 130.1; DB 9; Length 395;
Best Local Similarity 18.6% Pred. No. 97;
Matches 69; Conservative 21; Mismatches 51; Indels 229; Gaps 23;
Qy 6 GTGYNNG-----YF-----14
Db 43 GAGMNLGNLEAAVNGTPNETANGNPTYPELIKRYKAGFKSIRIPVSTLNNIGSAPNY 102
Qy 15 -----YSYWNNDG-----HGVYTYNNGPGGQPSVMSNSGNFVG-----48
Db 103 TINAAMLRIOQVVDVAY-NEGLYIINIHD-GYNSVCGMLLVN-----GGNQT 152
Qy 49 -----KGWOP-GTK-----NKVINFSGSY-NPN-----69
Db 153 IKKKYKVKVQOLATKESNYNDRLIFESMNEV-FDCNNGPNASAYTYNLNAYNOIFVDIV 210
Qy 70 -----GNS-----YLSVGSNRPLIEYIIVENFG-----TYN 97
Db 211 ROTGNNNAKWLVPQMNWNT-ID-YTVGNYGFTLPTDNYRSSAIDSSOKRIMISAHYVS 267
Qy 98 P-STGATKICEVTSDC-----SVDIYRTORVNOPSLI---130
Db 268 PMDFAGEBNGITQMGATSTNPAKKTWGOEDYLEQSFMSMYKFTYO--GYRVYVIGERG 325
Qy 131 --TATFYQ-----YVSVRN-----HRSSGSYNTAN 154
Db 326 SIDKTSYDSSNNYRAAYAKAVTAKAKYKMYVPVYDNGHNGHGFALPFRSNNTVTOON 385
Qy 155 HFNMAAOGL 164
Db 386 IINA-IMQGN 394

RESULT 48
US-10-155-400-3
Sequence 3, Application US/10155400
Publication No. US20030108988A1
GENERAL INFORMATION:
APPLICANT: DING, SHI-YOU

US-09-880-748-1554

ORGANISM: Homo sapiens

TYPE: PRT

LENGTH: 251

SEQ ID NO: 1554

SOFTWARE: PatentIn Ver. 2.0

NUMBER OF SEQ ID NOS: 3239

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2001-06-15

CURRENT FILING DATE: 2001-06-15

CURRENT APPLICATION NUMBER: US/09/880,748

Query Match 12.4% Score 129.9; DB 9; Length 251;
Best Local Similarity 15.5%; Pred. No. 48;
Matches 38; Conservative 23; Mismatches 33; Indels 151; Gaps 9;

OY 3 IOPG----- 6

DB 12 VOPGRSLRLSCAASEFTFSNYAMHWROAPGKGLEWVAVISYDGTYSYADSMKGRFTIS 71

OY 7 -----TGYNNGYFYSYNNDHGCGVTYNG--- 30

DB 72 RDNKSNLYLQMSLRAEDTAVYICARENYDSLGTGYN--YFDYWGOG--TLVTVSSGGGG 128

OY 31 -----PGQFSYVMSNSNGNEVGK--GMQ---PGTKNKVI 60

DB 129 SGGGGSGGGGSAQAVLTQPSDSCGTPGQRTISMSSGSGSNISNAVSWYQQLPGTASKLL 188

OY 61 NFGSYNPNG-----NSYLSYVGWSRNPLEYI-----VENEGTYNPST 100

DB 189 IYSNNLRPSGVPDRFSGSKSATSAALAIISGLQSEDEADYCAAMDDTLNAEYFG----- 242

OY 101 GATKL 105

DB 243 GGTKV 247

Search completed: July 1, 2003, 11:58:36
Job time : 56 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2003, 11:47:35 ; Search time 41 Seconds

(without alignments)
445.501 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045
Sequence: 1 OTIOPGTGYNNGYFYSYWD.....YQIVAVEGYSFGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	100.0	222	2 S39154	xylinase 1 - fungus
2	1045	100.0	223	2 S39883	endo-1,4-beta-xylo
3	1022	97.8	190	1 A44594	endo-1,4-beta-xylo
4	1005	96.2	190	1 A44585	endo-1,4-beta-xylo
5	996	95.3	190	1 A44593	endo-1,4-beta-xylo
6	767.8	73.5	241	2 S71473	endo-1,4-beta-xylo
7	705.9	67.6	219	2 S71472	endo-1,4-beta-xylo
8	702.5	67.2	232	2 JC7577	endo-1,4-beta-xylo
9	684.9	65.5	225	1 S57469	endo-1,4-beta-xylo
10	670.9	64.2	221	1 S57469	endo-1,4-beta-xylo
11	656.8	62.9	221	2 JC7307	endo-1,4-beta-xylo
12	614.9	58.8	227	2 S43919	endo-1,4-beta-xylo
13	597.4	57.2	333	1 JS0590	endo-1,4-beta-xylo
14	597.4	57.2	335	2 JS0590	endo-1,4-beta-xylo
15	577.5	55.3	644	1 I40712	endo-1,4-beta-xylo
16	568.3	54.4	197	1 A44587	endo-1,4-beta-xylo
17	540.9	51.8	661	1 S59633	endo-1,4-beta-xylo
18	536.3	51.3	241	2 T37005	endo-1,4-beta-xylo
19	533.2	51.0	240	1 JS0591	endo-1,4-beta-xylo
20	530.9	50.8	656	1 S59631	endo-1,4-beta-xylo
21	527.4	50.5	240	1 S47512	endo-1,4-beta-xylo
22	527.3	50.5	210	2 C83762	endo-1,4-beta-xylo
23	506.2	48.4	213	1 I40569	endo-1,4-beta-xylo
24	505.2	48.3	213	1 S01734	endo-1,4-beta-xylo
25	505.2	48.3	213	1 S48126	endo-1,4-beta-xylo
26	472.8	45.2	354	1 S51779	endo-1,4-beta-xylo
27	467.6	44.7	228	1 MMB5XP	endo-1,4-beta-xylo
28	458.7	43.9	261	1 S12745	endo-1,4-beta-xylo
29	448.8	42.9	511	1 J01935	endo-1,4-beta-xylo

30	446.9	42.8	229	2 S39155	xylinase 2 - fungus
31	440.4	42.1	209	2 JC4909	endo-1,4-beta-xylo
32	434	41.5	211	1 S48229	endo-1,4-beta-xylo
33	432	41.3	211	2 S49542	endo-1,4-beta-xylo
34	430.9	41.2	211	1 JC1198	endo-1,4-beta-xylo
35	410	39.2	954	1 S20907	endo-1,4-beta-xylo
36	402.8	38.5	789	2 S58235	endo-1,4-beta-xylo
37	392.5	37.6	802	2 A36910	xylinase, beta(1,3
38	386.2	37.0	781	2 S51592	xyNB precursor - R
39	316.1	30.2	607	2 S49528	endoxylinase - run
40	316.1	30.2	607	2 S24754	endo-1,4-beta-xylo
41	299.3	28.6	608	2 B53295	xylinase (EC 3.2.1
42	280	26.8	50	2 A61149	endo-1,4-beta-xylo
43	255.5	24.4	266	1 S48865	endo-1,4-beta-xylo
44	172.8	16.5	1441	2 A8685	prophage pil prote
45	170.9	16.4	2817	2 B97033	uncharacterized pr

ALIGNMENTS

RESULT 1
S39154
xylinase 1 - fungus (Trichoderma reesei)
C:Species: Trichoderma reesei
C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C:Accession: S39154
R:Roerstroem, A.; Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkkainen, N.; Harkki, A.; K
Biotechnology 10, 1461-1465, 1992
A>Title: The two major xylinases from Trichoderma reesei: characterization of both en
A:Reference number: S39154
A:Accession: S39154
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222 <TOE>
A:Cross-references: EMBL:X69573; NID:q396563; PIDN:CAA49293.1; PID:q396564
A:Genetics:
A:Gene: xyn1
A:Introns: 90/2
C:Superfamily: endo-1,4-beta-xylinase; endo-1,4-beta-xylinase homology
F:44-222/Domain: endo-1,4-beta-xylinase homology <XTL>

Query Match	100.0%	Score 1045	DB 2	Length 222
Best Local Similarity	100.0%	Pred. No. 3.7e-39		
Matches	190	Conservative	0	Mismatches 0; Indels 0; Gaps 0;

OY 1 OTIOPGTGYNNGYFYSYWDGCGVTTYNNGCGGFSVMSNSGNFVGCKGMOPTKMKVI 60
|||||
Db 33 OTIOPGTGYNNGYFYSYWDGCGVTTYNNGCGGFSVMSNSGNFVGCKGMOPTKMKVI 92
OY 61 NFSGSYNPNSGNSYLSVYGMSRNPPIEYIVENPGYVNPSTGATKLGVTSPGSVYDIYRT 120
|||||
Db 93 NFSGSYNPNSGNSYLSVYGMSRNPPIEYIVENPGYVNPSTGATKLGVTSPGSVYDIYRT 152
OY 121 ORVNOPSLITGATFYQYVSVRRNRSSGSVNTANHFNMAOQGLTMDYQIVAVEGYF 180
|||||
Db 153 ORVNOPSLITGATFYQYVSVRRNRSSGSVNTANHFNMAOQGLTMDYQIVAVEGYF 212
OY 181 SSGSASITVS 190
|||||
Db 213 SSGSASITVS 222

RESULT 2
S39883
endo-1,4-beta-xylinase (EC 3.2.1.8) II precursor - fungus (Trichoderma reesei)
N:Alternate names: endoxylinase II
C:Species: Trichoderma reesei
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C:Accession: S39883; S39884
R:Saarelainen, R.; Palomäki, M.; Fagerström, R.; Suominen, P.L.; Nevalainen, K.M.H.
Mol. Gen. Genet. 241, 497-503, 1993
A>Title: Cloning, sequencing and enhanced expression of the Trichoderma reesei endoxy

A:Reference number: S39883; MUID:94088442; PMID:8264524
A:Accession: S39883
A:Molecule type: DNA
A:Residues: 1-223 <SAA>
A:Cross-references: EMBL:567387; NID:9455906; PIDN:AB29346.1; PID:9455907
A:Experimental source: strain QM6a
A:Accession: S39884
A:Molecule type: protein
A:Residues: 34-43;49-57;121-151;178-191 <SAF>
C:Genetics:
A:Gene: xln2
A:Introns: 91/2
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-19/Domain: signal sequence #status predicted <PRO>
F:20-33/Domain: propeptide #status predicted <SIG>
F:34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>
F:45-223/Domain: endo-1,4-beta-xylanase homology <XYL>
F:71-94/Binding site: carbohydrate (asn) (covalent) #status predicted
F:110-121/Binding site: substrate (tyr) #status predicted
F:119-210/Active site: Glu #status predicted

Query Match 100.0%; Score 1045; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.8e-39;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OTTQPGTGNNGFYFYWMNDGHCGVYTTNGPGGQFVSVMNSNGNFVGKGMQPTKKNKYI 60
|||||
Db 34 OTTQPGTGNNGFYFYWMNDGHCGVYTTNGPGGQFVSVMNSNGNFVGKGMQPTKKNKYI 93
|||||
OY 61 NFGSYNPNNGNSLYSVYGMWRNPLIEYIYVENFGTNPSTGATKLGCVTSDGSVYDIYRT 120
|||||
Db 94 NFGSYNPNNGNSLYSVYGMWRNPLIEYIYVENFGTNPSTGATKLGCVTSDGSVYDIYRT 153
|||||
OY 121 QRVNPSIIIGTATFFYQWYSVRNRHSSGSVNTANHNANAAQGLTLGTMDYQIVAVEGYF 180
|||||
Db 154 QRVNPSIIIGTATFFYQWYSVRNRHSSGSVNTANHNANAAQGLTLGTMDYQIVAVEGYF 213
|||||
OY 181 SSGSASITVS 190
|||||
Db 214 SSGSASITVS 223

RESULT 3

A44594
endo-1,4-beta-xylanase (EC 3.2.1.8) IIA - fungus (Trichoderma viride)

N:Alternate names: xylanase IIA
C:Species: Trichoderma viride
C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 07-Nov-1997
C:Accession: A44594
R:Yaguchi, M.
submitted to the Protein Sequence Database, March 1994

A:Reference number: A44593
A:Accession: A44594
A:Molecule type: protein
A:Residues: 1-190 <YAG>

C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-190/Domain: endo-1,4-beta-xylanase homology <XYL>
F:17-88/Binding site: substrate (tyr) #status predicted
F:86-177/Active site: Glu #status predicted

Query Match 97.8%; Score 1022; DB 1; Length 190;
Best Local Similarity 97.4%; Pred. No. 2.8e-38;
Matches 185; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 OTTQPGTGNNGFYFYWMNDGHCGVYTTNGPGGQFVSVMNSNGNFVGKGMQPTKKNKYI 60

Db 1 OTTQPGTGNNGFYFYWMNDGHCGVYTTNGPGGQFVSVMNSNGNFVGKGMQPTKKNKYI 60
|||||
OY 61 NFGSYNPNNGNSLYSVYGMWRNPLIEYIYVENFGTNPSTGATKLGCVTSDGSVYDIYRT 120
|||||
Db 61 NFGSYNPNNGNSLYSVYGMWRNPLIEYIYVENFGTNPSTGATKLGCVTSDGSVYDIYRT 120
|||||
OY 121 QRVNPSIIIGTATFFYQWYSVRNRHSSGSVNTANHNANAAQGLTLGTMDYQIVAVEGYF 180
|||||
Db 121 QRVNPSIIIGTATFFYQWYSVRNRHSSGSVNTANHNANAAQGLTLGTMDYQIVAVEGYF 180
|||||
OY 181 SSGSASITVS 190
|||||
Db 181 SSGSASITVS 190

RESULT 4

A44595
endo-1,4-beta-xylanase (EC 3.2.1.8) IIB (proteinase-sensitive) - fungus (Trichoderma

N:Alternate names: xylanase IIB
C:Species: Trichoderma viride
C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 13-Mar-1998
C:Accession: A44595
R:Yaguchi, M.
submitted to the Protein Sequence Database, March 1994

A:Reference number: A44593
A:Accession: A44595
A:Status: preliminary

A:Molecule type: protein
A:Residues: 1-190 <YAG>

C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
F:86-177/Active site: Glu #status predicted
F:126-127/Cleavage site: Pro-Ser (unidentified proteinase) #status predicted
F:129-130/Cleavage site: Glu-Gly (unidentified proteinase)

Query Match 96.2%; Score 1005; DB 1; Length 190;
Best Local Similarity 95.8%; Pred. No. 1.6e-37;
Matches 182; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 OTTQPGTGNNGFYFYWMNDGHCGVYTTNGPGGQFVSVMNSNGNFVGKGMQPTKKNKYI 60
|||||
Db 1 OTTQPGTGNNGFYFYWMNDGHCGVYTTNGPGGQFVSVMNSNGNFVGKGMQPTKKNKYI 60
|||||
OY 61 NFGSYNPNNGNSLYSVYGMWRNPLIEYIYVENFGTNPSTGATKLGCVTSDGSVYDIYRT 120
|||||
Db 61 NFGSYNPNNGNSLYSVYGMWRNPLIEYIYVENFGTNPSTGATKLGCVTSDGSVYDIYRT 120
|||||
OY 121 QRVNPSIIIGTATFFYQWYSVRNRHSSGSVNTANHNANAAQGLTLGTMDYQIVAVEGYF 180
|||||
Db 121 QRVNPSIIIGTATFFYQWYSVRNRHSSGSVNTANHNANAAQGLTLGTMDYQIVAVEGYF 180
|||||
OY 181 SSGSASITVS 190
|||||
Db 181 SSGSASITVS 190

RESULT 5

A44593
endo-1,4-beta-xylanase (EC 3.2.1.8) [validated] - fungus (Trichoderma harzianum) (str

N:Alternate names: xylanase
C:Species: Trichoderma harzianum
C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Sep-2000
C:Accession: A44593
R:Yaguchi, M.
submitted to the Protein Sequence Database, March 1994

A:Reference number: A44593
A:Accession: A44593
A:Molecule type: protein

A:Title: Novel cellulose-binding domains, NodB homologues and conserved modular architected
A:Reference number: S59631; MUID:96077124; PMID:749233
A:Accession: S59631
A:Molecule type: DNA
A:Residues: 1-656 <MIL>
A:Cross-References: EMBL:248925; NID:g757806; PIDN:CAA88761.1; PID:g757807
C:Genetics:
A:Gene: xynA
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: Pseudomonas endo-1,4-beta-xylanase E; endo-1,4-beta-xylanase homology; 91
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-656/Product: endo-1,4-beta-xylanase A #status predicted <MAT>
F:40-225/Domain: endo-1,4-beta-xylanase homology <XYL>
F:398-544/Domain: nodB homology <NODB>
F:611-648/Domain: glycosidase GwGw domain homology <GwG>
F:115,212/Active site: Glu #status predicted

Query Match 50.8%; Score 530.9; DB 1; Length 656;
Best Local Similarity 51.8%; Pred. No. 1,2e-15;
Matches 100; Conservative 36; Mismatches 46; Indels 11; Gaps 6;

QY 7 TGYNNGFYSYWNDGHCYTYTNGPGQFSVWMSN-SGNFVGKGWQPGTKRKVINFGS 65
DB 35 TGHNGFYTFMKDS-GDASMGLOAGGRITQMSNTNMWVGKGNPCGP-KVYIYSGS 92
QY 66 YNPNG--NSYLSVYGSRNPLIEYIVENFTYNS--TGATKLGWISDGSVYDIYRQ 121
DB 93 YVNDSONSYLALYGTWRSPLIEYIYESYSGSNPASCGSDYDYGFSODGATYVNRQ 152
QY 122 RVNPSITGATFYQWYSRRNHR--SGSVNTANHPNMAOGLTGTMDYOYAVE 177
DB 153 RVQPSIDGTQTFYQYFVRSRKRKGGQITTTANHPNMAKGLNHNHYAVLATE 212
QY 178 GFSSGSASITVS 190
DB 213 GYOSRGSIDITVS 225

RESULT 21

endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - Streptomyces sp.

N:Alternate names: xylanase
C:Species: Streptomyces sp.
C:Date: 13-Jan-1995 #sequence_revision 22-Nov-1996 #text_change 18-Jun-1999
C:Accession: S47512
R:Maizy-Servais, C.; Moreau, A.; Gerard, C.; Dusart, J.
Submitted to the EMBL Data Library, August 1994
A:Description: Cloning and sequencing of a xylanase-encoding gene from Streptomyces sp.
A:Reference number: S47512
A:Accession: S47512
A:Molecule type: DNA
A:Residues: 1-240 <MAZ>
A:Cross-References: EMBL:X81045; NID:9531767; PIDN:CAA56935.1; PID:9531768
A:Experimental source: strain EC3
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-47/Domain: signal sequence #status predicted <SIG>
F:48-240/Product: endo-1,4-beta-xylanase #status predicted <MAT>
F:62-239/Domain: endo-1,4-beta-xylanase homology <XYL>
F:135,226/Active site: Glu #status predicted

Query Match 50.5%; Score 527.4; DB 1; Length 240;
Best Local Similarity 53.8%; Pred. No. 2.3e-16;
Matches 100; Conservative 31; Mismatches 49; Indels 6; Gaps 6;

QY 7 TGYNNGFYSYWNDGHCYTYTNGPGQFSVWMSN-SGNFVGKGWQPGTKRKVINFGS 66

DB 58 TGY-GGMYSEFWTDGGSYSMTLNGGYSYSTQWTCNGNEFVACKGNGGR-RTVYSGYF 115
QY 67 NPNGNSYLSVYGSRNPLIEYIVENFTYNSGTATKLGWISDGSVYDIYRQVNP 126
DB 116 NPNGNGYGLYGTWTSPLIEYIVDNWGSYR-TSEYR-GTYSDGTYDIYKTRRYNP 173
QY 127 STIGTATFYQWYSVRNRH-RSSGSVNTANHPNMAOGLTGTMD-YOIVAEYGFSSGS 184
DB 174 SVETRTFQYVSVQSKYISGTTTGNHFPNMAKGNLQFGQYMTMATEGVOSSS 233
QY 185 ASITVS 190
DB 234 SMITVS 239

RESULT 22

endo-1,4-beta-xylanhydrolase BH0899 (Imported) - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: C83762
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: C83762
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-210 <STO>
A:Cross-References: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BA804618.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0899
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

Query Match 50.5%; Score 527.3; DB 2; Length 210;
Best Local Similarity 52.5%; Pred. No. 1.8e-16;
Matches 95; Conservative 33; Mismatches 46; Indels 7; Gaps 4;

QY 14 FYSYNDGHCYTYTNGPGQFSVWMSN-SGNFVGKGWQPGTKRKVINFGS 72
DB 31 YWQYMTDGGTYNATNGPGNYSVTWRDGNFVKGWISGPNRTIHNACWEPSCNG 90
QY 73 YLSVYGSRNPLIEYIVENFTYNSGTATKLGWISDGSVYDIYRQVNPISITGA 132
DB 91 YLTLYGTWTSPLIEYIVDNWGTYRPT-GTHRGVYSDGTYDIYTRRYNAPSIDGTQ 148
QY 133 TFQYVSVRNRHRSRG--SVNTANHPNMAOGLTGTMDYQIVAEYGFSSGSASIT 188
DB 149 TFQFVSVRNRHRSRGPNNNYSITFNSHNVRNMAKGNLGSMSYQVILATEGYSSGRSVNT 208
QY 189 V 189
DB 209 V 209

RESULT 23

endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Bacillus subtilis

N:Alternate names: xylanase A
C:Species: Bacillus subtilis
C:Date: 12-Aug-1996 #sequence_revision 02-Jul-1998 #text_change 21-Jul-2000
C:Accession: I40569; S39157; S39158; A53635; F69735; S51711
R:Wolf, M.; Geczi, A.; Simon, O.; Borriass, R.
Microbiology 141, 281-290, 1995
A:Title: Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis
A:Reference number: I40370; MUID:95219081; PMID:7704256
A:Accession: I40569
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-22, 24-213 <WOL>
A:Cross-References: EMBL:Z34519; NID:g2995396; PIDN:CAA84276.1; PID:9607050

Db 211 YQSSGSANV 219

RESULT 28

S12745

endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Clostridium acetobutylicum

N:Alternate names: xylanase B

C:Species: Clostridium acetobutylicum

C>Date: 30-Sep-1993 #sequence_revision 22-Nov-1996 #text_change 18-Jun-1999

C:Accession: S12745

R:Zappe, H.; Jones, W.A.; Woods, D.R.

Nucleic Acids Res. 18, 2179, 1990

A:Title: Nucleotide sequence of a Clostridium acetobutylicum P262 xylanase gene (xynB).

A:Reference number: S12745; MUID:90245673; PMID:2336398

A:Accession: S12745

A:Molecule type: DNA

A:Residues: 1-261 <ZAP>

A:Cross-references: EMBL:M31726; NID:g144933; PIDN:AAA23287.1; PID:g144934

A:Experimental source: strain P262

C:Genetics:

A:Gene: xynB

C:Function:

A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A:Pathway: xylan degradation

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-261/Product: endo-1,4-beta-xylanase B #status predicted <MAT>

F:72-255/Domain: endo-1,4-beta-xylanase homology <XLY>

F:152-242/Active site: Glu #status predicted

Query Match 43.9%; Score 458.7; DB 1; Length 261;

Best Local Similarity 47.1%; Pred. No. 2,9e-13;

Matches 89; Conservative 27; Mismatches 60; Indels 13; Gaps 4;

OY 8 GYNGCYFYSYWNDGCGVYTYNGPGGQFSVMNSGNGFVCGKG-----WDGTRNK 58

Db 68 GNGCYDYELMKD-YGNTSMFLKNGCAFSCQMSNGMLFRKKGKNDQTYKLG--NI 124

OY 59 VINFGSYNPNNGNSLYSYGMSRNPLIEYIYENGTNPISGATKLGCVSDGSVDYIR 118

Db 125 SVNDCNTPYGNNSYLCLYGVMTSPLEVEYIVDSGMSRPPGTSK-GTITVDGSGIYDIY 183

OY 119 RTQVNPQSIIGTATFYQYWSVRRNRSSGSVNTAHNANAQGLTGTMDYQVAVEG 178

Db 184 ETRINQDSIOGNTTFKQYWSVRTRKRTSGTISVSKHFAWDSKMPLGKMHETAFNIEG 243

OY 179 YFSSGSAST 187

Db 244 YQSSGKADV 252

RESULT 29

J01935

endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Clostridium stercoararium

N:Alternate names: xylanase A

C:Species: Clostridium stercoararium

C>Date: 30-Sep-1993 #sequence_revision 22-Nov-1996 #text_change 26-Feb-1999

C:Accession: J01935; P00531

R:Sakka, K.; Kojima, Y.; Kondo, T.; Karita, S.I.; Ohmiya, K.; Shimada, K.

Biosci. Biotechnol. Biochem. 57, 273-277, 1993

A:Title: Nucleotide sequence of the Clostridium stercoararium xyna gene encoding xylanase

A:Reference number: J01935; MUID:93214115; PMID:7763496

A:Accession: J01935

A:Molecule type: DNA

A:Residues: 1-511 <SAK>

A:Accession: P00531

A:Molecule type: protein

A:Residues: 31-40 <SA2>

A>Note: the authors translated the codon AAC for residue 415 as Gly

C:Function:

A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A:Pathway: xylan degradation

C:Superfamily: Clostridium endo-1,4-beta-xylanase A; Clostridium xylanase A repeat ho

C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-511/Product: endo-1,4-beta-xylanase A #status predicted <MAT>

F:44-228/Domain: endo-1,4-beta-xylanase homology <XLY>

F:236-244/Region: linker

F:273-368/Domain: Clostridium xylanase A repeat homology <CXAX>

F:413-506/Domain: Clostridium xylanase A repeat homology <CXAX>

F:124,215/Active site: Glu #status predicted

Query Match 42.9%; Score 448.8; DB 1; Length 511;

Best Local Similarity 46.2%; Pred. No. 3e-12;

Matches 90; Conservative 24; Mismatches 59; Indels 22; Gaps 5;

OY 7 TGYNNGCYFYSYWNDGCGVYTYNGGQFSVMNSGNGFVCGKGQPGTKKK----- 58

Db 39 TGTGCGDYELMKD-YGNTIMELNDGTFSCQMSNGMLFRKG-----RRFNSDKTYQ 91

OY 59 -----VINFGSYNPNNGNSLYSYGMSRNPLIEYIYENGTNPISGATKLGCVTS-DG 112

Db 92 ELGDIVVERGCDYENNGNSYLCLYGVMTSPLEVEYIVDSGMSRPPGTSKGTITVDG 150

OY 113 SVYDIYRTQVNPQSIIGTATFYQYWSVRRNRSSGSVNTAHNANAQGLTGTMDYQ 172

Db 151 GYIEIYETTRVNPQSIIGTATFYQYWSVRRNRSSGSVNTAHNANAQGLTGTMDYQ 210

OY 173 IVAVCGYFSSGSAST 187

Db 211 ALTEGQYSSGSYANV 225

RESULT 30

S39155

xylanase 2 - fungus (Trichoderma reesei)

C:Species: Trichoderma reesei

C>Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999

C:Accession: S39155

R:Toerrien, A.; Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkinen, N.; Harkki, A.; K

Biotechnology 10, 1461-1465, 1992

A:Title: The two major xylanases from trichoderma reesei: characterization of both en

A:Reference number: S39154

A:Accession: S39155

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-229 <TOR>

A:Cross-references: EMBL:X69574; NID:g3396565; PIDN:CAA49294.1; PID:g3396566

C:Genetics:

A:Gene: xyn2

A:Introns: 97/2

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

F:53-228/Domain: endo-1,4-beta-xylanase homology <XLY>

Query Match 42.8%; Score 446.9; DB 2; Length 229;

Best Local Similarity 51.3%; Pred. No. 7.3e-13;

Matches 98; Conservative 22; Mismatches 50; Indels 21; Gaps 6;

OY 1 OTIQPGCYFYSYWNDGCGVYTYNGGQFSVMNSGNGFVCGKGQPGTKKNVI 60

Db 58 QNYQYG-----GOVSYSPSNTG-FSVWMTQDDFVVGWMTGS-SAPI 99

OY 61 NFSGYNPN-GNSYLSYGMSRNPLIEYIYENGTNPISGATKLGCVSDGSVDYIR 119

Db 100 NFGSGFSVNSGTLGLSVGMSNPLVEYIYEDNINY-PAQGYK-GTIVSDGATYTTWE 157

OY 120 TORVNPQSIIGTATFYQYWSVRRNRSSGSVNTAHNANAQGLTGTMDYQVAVEGY 179

Db 158 NTRVNEPSIQGTATFQYISVRRNSPRTSGTIVQHHFNAMASLGHLGQMMYQVAVEGW 217

OY 180 FSSGSASTVS 190

Db 218 GQSGASQSSVS 228


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RESULT 40
S24754
endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - rumen fungus (Neocallimastix patriciarum)
N:Alternate names: xylanase A
C:Species: Neocallimastix patriciarum
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Oct-1999
C:Accession: S24754; S21392
R:Gillbert, H.J.; Hazlewood, G.P.; Laurie, J.I.; Orpin, C.G.; Xue, G.P.
Mol. Microbiol. 6, 2065-2072, 1992
A:Title: Homologous catalytic domains in a rumen fungal xylanase: evidence for gene dupl
A:Reference number: S24754; MUID:93023832; PMID:1406248
A:Accession: S24754
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-607 <GIL>
A:Cross-references: EMBL:X65526
R:Gillbert, H.J.; Hazlewood, G.P.; Laurie, J.I.; Orpin, C.G.; Xue, G.P.
submitted to the EMBL Data Library, April 1992
A:Description: Homologous catalytic domains in a rumen fungal xylanase: evidence for gen
A:Reference number: S21392
A:Accession: S21392
A:Molecule type: mRNA
A:Residues: 1-152, 'S', 154-607 <GIL>
A:Cross-references: EMBL:X65526; MID:93090; PIDN:CAA46498.1; PID:93091
C:Genetics:
A:Gene: xyna
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic linkages in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-607/Product: endo-1,4-beta-xylanase #status predicted <MAT>
F:46-242/Domain: endo-1,4-beta-xylanase homology <XYL1>
F:291-487/Domain: endo-1,4-beta-xylanase homology <XYL2>

Query Match          30.2%; Score 316.1; DB 2; Length 607;
Best Local Similarity 34.0%; Pred. No. 2.8e-06;
Matches 69; Conservative 38; Mismatches 72; Indels 24; Gaps 6;

QY 8 GYNNCFYSYNNNDGHC-VTTYNGPGGPFVNMWNS-NSGNFVGSKMQPGTKNV---- 59
DB 287 GYNNDFSYEIMLDNNGMGSMGLGATFKAEMNAAVNRGNFLARGLDFGSGKATDYD 346
QY 60 ---INFSQSY---NPNNSYLSYVGMNRN-----PLEXYIVNFCGTYNSTATRLG 106
DB 347 YIGLDYAAIVKOTASASGNSRLCYIGMFONRGLNGVPLVEYIITEDWVDPDAOGKM-- 404
QY 107 EVTSDGSYYDIYRTQRVNOPSIICTATFYQYWSVRNRHSSGSVYTAHFNAHMAOQGLTL 166
DB 405 -VTIDGAGYKIFQMDHTGPTINGSETFKQYFSVRQKRTSHIIVSDHFKEMAGQNGI 463
QY 167 GTMDYQIVAVEGYSFSSGSASITV 189
DB 464 GNLVEVALNAEGWSSGVADYTL 486

RESULT 41
BS3295
xylanase (EC 3.2.1.-) precursor - Fibrobacter succinogenes
C:Species: Fibrobacter succinogenes
C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 08-Oct-1999
C:Accession: BS3295
R:Paradis, F.W.; Zhu, H.; Krell, P.J.; Phillips, J.P.; Forberg, C.W.
J. Bacteriol. 175, 7666-7672, 1993
A:Title: The xynC gene from Fibrobacter succinogenes S85 codes for a xylanase with two s
A:Reference number: AS3295; MUID:94064561; PMID:8244936
A:Accession: BS3295
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-608 <PAR>
A:Cross-references: GB:U01037; NID:9402870; PIDN:AAA21848.1; PID:9402871
```

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C:Genetics:
A:Gene: xynC
C:Superfamily: endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase
F:51-250/Domain: endo-1,4-beta-xylanase homology <XYL1>
F:327-514/Domain: endo-1,4-beta-xylanase homology <XYL2>

Query Match          28.6%; Score 299.3; DB 2; Length 608;
Best Local Similarity 33.0%; Pred. No. 1.5e-05;
Matches 69; Conservative 32; Mismatches 71; Indels 37; Gaps 7;

QY 8 GYNNG-----YFYSYNNNDGHCYTYNNGPGGPFVNMWNSGNFVGSKMQPGTKN 57
DB 313 GNNNSYTVGNVSSPYHVEIYVQC-GNNSMTFYDNGTKASWNGTNDFLARGEFKYDEKH 371
QY 58 KVINP-----SSGYNNNGSYLSYVGMNSNPLEXYIVNFCGTYNSTGAT 103
DB 372 TYEELGPIDAYYKWSKSGAGYN---YIGYGVTDVPLVEYIIVDW--FN-KPGAN 423
QY 104 KL---GEVTSYDGSYYDIYRTQRVNOPSIICTATFYQYWSVRNRHSSGSVYTAHFNAH 159
DB 424 LLGQRKGFEYTDGDTYELWMTNRVQGPSIKGTQFPQYFSVRKASRSGCHIDITAHMKKM 483
QY 160 AQQGLTCTMDYQIVAVEGYSFSSGSASITV 188
DB 484 EELGKMKGMKMYEAKVLEAGSGSGSFVDT 512

RESULT 42
A61149
endo-1,4-beta-xylanase (EC 3.2.1.8) - fungus (Trichoderma viride) (fragment)
C:Species: Trichoderma viride
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 31-Jan-1997
C:Accession: A61149
R:Ujite, M.; Roy, C.; Yaguchi, M.
Appl. Environ. Microbiol. 57, 1860-1862, 1991
A:Title: Low-molecular-weight xylanase from Trichoderma viride.
A:Reference number: A61149; MUID:91336731; PMID:1872616
A:Accession: A61149
A:Molecule type: protein
A:Residues: 1-50 <UJT>
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic linkages in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation; pyroglyluamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match          26.8%; Score 280; DB 2; Length 50;
Best Local Similarity 94.0%; Pred. No. 7.6e-07;
Matches 47; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTIQPGCTYNNGYFYSYNNNDGHCYTYNNGPGGPFVNMWNSGNFVGSKG 50
DB 1 OSIGPGTGTFNNGYFYSYNNNDGHCYTYNNGPGGPFVNMWNSGNFVGSKG 50

RESULT 43
S48865
endo-1,4-beta-xylanase (EC 3.2.1.8) 2 precursor - rumen fungus (Neocallimastix fronta)
N:Alternate names: xylanase 2
C:Species: Neocallimastix frontalis
C>Date: 13-Jan-1995 #sequence_revision 22-Nov-1996 #text_change 18-Jun-1999
C:Accession: S48865
R:Durand, R.; Fevre, M.
submitted to the EMBL Data Library, November 1994
A:Description: The xyn2 gene of the anaerobic fungus Neocallimastix frontalis.
A:Reference number: S48865
A:Accession: S48865
A:Molecule type: mRNA
A:Residues: 1-266 <DUR>
A:Cross-references: EMBL:X82439; NID:9565625; PIDN:CA57820.1; PID:9565626
C:Genetics:
```


Db 1250 YXSDNNGIMLTGLQILINGLYCFCNSDSGSKTGLVLTLYGKTYYPDSYSVSGFQINNNNTY 1309
OY 50 -----GMP-----GTRKVINFGSSY-- 66
Db 1310 YFGNDGTMTGWNVNGYRYRYLNDGSIKATGMQTTIDGKNKYFDYIGAKTGVINDIDNTYG 1369
OY 67 -----NPNNGSY- 73
Db 1370 FNNSGVMLTGMQHINGSTYFNSNGIANTGFTLYLGKTYFPDSYGRMOTISMTINTSTY 1429
OY 74 -----LSYFGMSRNPLEYIYVENFT----- 95
Db 1430 FYANGVMKTSTDPMTLAV-GWVRDSYXYQYLYLMAAGTKLTGLQITDGNNTYFDSNGIMQ 1488
OY 96 -----YNPSGATKLGENVSDGSVY--DIYROR 122
Db 1489 TGLITINGRIGFYGVNGWMLYGLQFINNTFYNSYISQTFPLSGTTFYFDSYGEKR 1548
OY 123 V-----NPSI----- 128
Db 1549 IGLTYINNYYFNSGIMETGMISLYRYANPNGLITGFTINGKTYFNSDGLIYDL 1608
OY 129 -----IGATFY-----OYWSYRNH 144
Db 1609 QYNGSYGFDKNGWMLYGLQITIGNTYLNNGISQSGFTLNGKTYFDSYGMRTGI 1668
OY 145 RS-----SGSVNT-----AN-----HFNMAAQ----- 161
Db 1669 QVINNNYFFGDNGLQITGWMISODNLRYANSSGCLTGLQITIDGKKYFNSYARRETGL 1728
OY 162 -----OG----- 163
Db 1729 VYINNTYGFNDGTLTYSWMHINNGRMCFNTDGYTKTGMVYLGKSCVLDSSQGLSTNG 1788
OY 164 -LTLG-----TMDQIYAVEGTFSSGSA 185
Db 1789 LTTIGHNIYFFGSDYSMTK--GMVTSGSS 1815

RESULT 46

S76412
hypothetical protein slr0408 - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #extL_change 20-Jun-2000
C:Accession: S76412
R:Kaneko, T.; Sato, S.; Kottani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
S.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76412
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4199 <KAN>
A:Cross-references: EMBL:D90915; GB:AB001339; NID:q1653604; PIDs:BAI18541.1; PID:q165362
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: *Synechocystis* hypothetical protein slr0408

Query Match 15.9%; Score 166.3; DB 2; Length 4199;
Best Local Similarity 10.8%; Pred. No. 5e+02;
Matches 78; Conservative 29; Mismatches 65; Indels 547; Gaps 19;
OY 1 OTIOPG-----TGYNNGYFYSWNDGHGVYTTNGPG 32
Db 3010 OTIOMGGDQANQVATNWNSSHPRAVLGOSNGDIWY-----PG 3056
OY 33 G-----QFSVNSNSGN-----FVGKKG----- 50
Db 3057 GNONMSGCKLPAETINELAVNMNNTSGNPOTIAGLGKGIIEYNGSTWVNGNPGYOGDGR 3116
OY 51 -----WQPGTKN 57

Db 3117 SAITQAMAVQWGEDGSSPQLVGLADGAVIYNTQSGMRTINNFKSKVTOLSVQMOEASNP 3176
OY 58 KYI----- 60
Db 3177 NIVGLDNSEVOYQYQSGNCGWMTQPHDDGKNVYEVQOLAVQMTSDAOPLYVGLGDGNGN 3236
OY 61 -----NFGSGYNPNGN----- 71
Db 3237 GSWYTYQSGEGGQWTFLSGLPSCAALQAMAVQWNFSSSPNPNVNDLKYVGQADSTV 3296
OY 72 SYLSYVQMSRNP.LI-----EY----- 87
Db 3297 SYNCGNMTATPAINSLIQITLNAITVQSANQPQITVGLGDEYDNGQLWYLPNPQO 3356
OY 88 -----YIVENFTYNS-----TGA-----TKL 105
Db 3357 SMOELGSVNVASPIQTQIDSSWTESLVPNSQTDNLVYFFGSDPNDYVNTGTIGDDVAV 3416
OY 106 GEVTSQD-----GSVYDIYRQ----- 121
Db 3417 GSATGESFLAGGDDQILTKGLDVVYAGPGDWVSVSDTYFRRLNGTGFDILALQYN 3476
OY 122 -----RVNPSIIGTAT----- 133
Db 3477 GQNMDLTTLSPGLRLQDFETIDIRQYGANQLTLNLSVNLSSNMTVILMDESGDSLQ 3536
OY 134 -----FYQYS----- 139
Db 3537 SSDFGADGTTYQYQGRFYQYKSSNSAIVLVNQPTMPSPFTAPSONKPOPLPNCNCTSN 3596
OY 140 --VRRNHRSSGSVNAN-----HFNMAAQGLT----- 165
Db 3597 AALNTNINANTGANANGNFENDENINTGNANTGNFN-----NGNTNMGVGDININATLFPSS 3652
OY 166 -----LGTMDYQI-----VAVEGYFSSGSASTYV 189
Db 3653 PTASEALGEVDFTIERTGDLDRKYVYVSYLTQMDMGAGDRLYPVAGQLVFKRGEIKRTI 3711

RESULT 47

A42296
lysozyme 2 (EC 3.2.1.1) precursor - *Enterococcus hirae* (ATCC 9790)
C:Species: *Enterococcus hirae*
C:Date: 10-Jul-1992 #sequence_revision 18-Sep-1992 #extL_change 15-Oct-1999
C:Accession: A42296
R:Chu, C.P.; Kariyama, R.; Daneo-Moore, L.; Shockman, G.D.
J. Bacteriol. 174, 1619-1625, 1992
A:Title: Cloning and sequence analysis of the muramidase-2 gene from *Enterococcus hir*
A:Reference number: A42296; MUID:92165737; PMID:1347040
A:Accession: A42296
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-666 <CHU>
A:Cross-references: GB:M7639; NID:q148303; PIDs:AA424776.1; PID:q148304
A:Note: the authors translated the codon GGT for residue 171 as Tyr
C:Keywords: glycosidase; hydrolase

Query Match 15.7%; Score 163.6; DB 2; Length 666;
Best Local Similarity 17.5%; Pred. No. 17;
Matches 70; Conservative 28; Mismatches 68; Indels 234; Gaps 16;
OY 7 TGYNNGYFY-SYW-----N 19
Db 161 TSGMGYVYAGTWKSNTKSYTDATACLTGRYATDPGYACKLNNITTYGLTKRYVTPASGN 220
OY 20 DGHGCVTYTNGPG-GQFSVNSNSGNFVCGKGMOPCT----- 55
Db 221 AG-GGVYTCNGGNTGTNTSNGSGTSGN-SGGSATTTGTTTYVSGDSYMGISHSFGITMAQ 278
OY 56 -----KNKVI-----NFGSYNPNNGS----- 72
Db 279 LIEMNNIKNNFIYPQOKLTIKGGQSGASTTNTGNASSGNTSGNTNTSGSTGQATGAKY 338

QY 73 -----YLSVGMNRNPLEIYIVENFGTY-----NPSTGAT 103
Db 339 TYKSGDSVWKIANDHDSINNOLEMMNNINNFYPCGOQLVSKSSSASSTSTNTGTNT 398
QY 104 -----KLGEVTSDCSVYDIYFRQVNOPSLIGATFYQVSVRR----- 142
Db 399 SSNTANTGSTTS-GSTYTYVKGESV-----WSVSNKFGISMNQLOIWNNIK 443
QY 143 -----NHRSSGSVNTANHFN-----ANA---Q 161
Db 444 NNFYQGLLYKGGSSSSNASTSTANNKNTASSNTSPTATGATYTVKAGESVWGVANK 503
QY 162 OGTLTGTM-----DYQIVAVEFYSSGSASITV 189
Db 504 NGISMNQLIEMNNIKNNFYPOGKLYVKGSSKASATATI 543
RESULT 48
D70575
Probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #extl_change 22-Oct-1999
C:Accession: D70575
R:Colo, S.T.; Brosch, R.; Parhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MID:98295987; PMID:9634230
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-3300 <CO>
A:Cross-references: GB:295324; GB:AL123456; NID:93261760; PIDN:CAB08587.1; PID:el299834;
A:Experimental source: strain H37RV
A:Genetics:
A:Gene: PPE
Query Match 15.7%; Score 163.6; DB 2; Length 3300;
Best Local Similarity 12.4%; Pred. No. 4e+02;
Matches 65; Conservative 37; Mismatches 57; Indels 364; Gaps 18;
QY 2 TTPOGTGYN-----GYF-----YSYND-- 20
Db 1844 TTTPSGFNNAGTGVSGVGNVSGNSGFFNLITSGSSGIGVGNFGLITSGFNFNTVS 1903
QY 21 ----- 20
Db 1904 GLVNSTGLISMPANLISGGNNGATVAGFVNNTQILNLGFGNVSGNVGHGNIIDSNVGL 1963
QY 21 -----GHGGV-----TYTNGP-----GGQSVNM 39
Db 1964 GNLGNANVGHGNIENFSSGNRGSYNTIPANLGNINIGLNLGISTNFGNAGDFNLGE 2023
QY 40 SNSGN-----FVGGK-- 50
Db 2024 ANSGSNNGIFANTGNNNIGIGLSGHQGEFSGNSNSTANTGLENSTNNIGLENSGTNI 2083
QY 51 -----WQPTKKKVINFGSYNPN-----NS 72
Db 2084 GIGNSGIGTIGNPGVNTGLNSGTGMGLNPNPOTGMVANNVGTNTGTYNTGYNVOSTNT 2143
QY 73 YLSVGMNRNPLEIYIVENFGTYNPSTGATKGEVTSDCSV-----YD--TYRNO 121
Db 2144 GIANVG-----IANTGSY--TOSTNTGS--NDGDRPTGTYNTGTYNTG 2189
QY 122 RVNOPSITGATFYQVSVRRNHRSSGSVNTANHFNA--AOQGLT-- 166
Db 2190 DVNTGAFIC-----GNFSNGATWQSDHOGCGAHYAITYTPQPLNLSNITPV 2237
QY 167 -----GTM--DYQIVAV----- 176

Db 2238 NPIHDLFGTLAVNGQIPATILRALGVTHFSVGIPIVRIAGTLPEVIDINIGDPGSSS 2297
QY 177 -----EGFSSGSAS 186
Db 2298 IPITTSAGPVVPLLDIPAPAGFNGSTTGPSSGFFNSGTGS 2240
RESULT 49
JP0001
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Rhizopus oryzae
N:Alternate names: 1,4-alpha-D-glucan glucosylidrolase; glucosylase
C:Species: Rhizopus oryzae
C:Date: 28-Dec-1987 #sequence_revision 23-Aug-1996 #extl_change 16-Jun-2000
C:Accession: JP0001
R:Ashikari, T.; Nakamura, N.; Tanaka, Y.; Kiuchi, N.; Shibano, Y.; Tanaka, T.; Amachi
Agric. Biol. Chem. 50, 957-964, 1986
A>Title: Rhizopus raw-starch-degrading glucosylase: its cloning and expression in ye
A:Reference number: A90022
A:Accession: JP0001
A:Molecule type: DNA
A:Residues: 1-604 <ASH>
A:Cross-references: GB:D00049; PIDN:BA00033.1; PID:9218035
A:Experimental source: strain SAM0034
A:Note: there are two errors in the published sequence (personal communication): GCT
Y to the known amino acid sequence of 11 peptides from glucosylase, including the am
R: Tanaka, Y.; Ashikari, T.; Nakamura, N.; Kiuchi, N.; Shibano, Y.; Amachi, T.; Yoshiz
Agric. Biol. Chem. 50, 965-969, 1980
A>Title: Comparison of amino acid sequences of three glucosylases and their structur
A:Reference number: A90023
A:Contents: annotation; homology; predicted secondary structure
A:Comment: Rhizopus glucosylase exists in multiple forms, Gluc 1, Gluc 2, and Gluc 3
C:Genetics:
A:Intons: 51/3; 110/3; 129/1; 436/3
C:Superfamily: Rhizopus glucan 1,4-alpha-glucosidase; glucan 1,4-alpha-glucosidase ho
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-604/Product: glucan 1,4-alpha-glucosidase (Gluc 1) #status predicted <GL1>
F:34-138/Domain: glucosylase starch-binding domain homology <SBD>
F:116-604/Product: (or 110-604) glucan 1,4-alpha-glucosidase (Gluc 3) #status predict
F:159-604/Product: glucan 1,4-alpha-glucosidase (Gluc 2) #status predicted <GL2>
F:166-592/Domain: glucan 1,4-alpha-glucosidase homology <GAC>
Query Match 15.2%; Score 159.3; DB 1; Length 604;
Best Local Similarity 10.0%; Pred. No. 21;
Matches 69; Conservative 25; Mismatches 70; Indels 267; Gaps 17;
QY 13 YF-----YSYNDGHGG-----VTYNGPGGFSVNM 39
Db 18 YFSLVSAASIPSSASVQQLDSYNYDSTPFGSKTYVKNIAVSKRVYIYADG-----SDNW 72
QY 40 SNSGNVGGKGNP--GTRKNVINFGSYN----- 67
Db 73 NNNGNITIASYSAPISGSNVEYWTFSASINGIKEFYIKVSGKTYYYDNNNSANYOVSTS 132
QY 68 -----PNGNSYLS----- 75
Db 133 KPPTTATATTTTAPSTSTTTPSSSEPAFTPTGNTSTISWIKQGISRFAMLRNINP 192
QY 76 -----YVGMNRNPLI-----EY-----YIVENFG 94
Db 193 GSATGFIASLSTAGPDYIYAWTRDAALTSNVIYEVNTLSGNKTLNLVLDYVFSVK 252
QY 95 TYNPSTGARKLGE--VTSGSVY-----DIYRQVRNOPSLI 129
Db 253 TOSTSTVNCCLDEPKFNPDGSGTGMGRPQNDGPAERATFTILFADSYLTOTKDAASYT 312
QY 130 GT--ATF-----YQYV-----SVPR 142
Db 313 GILKRAIFRDLDDYVNVWNSNGCFDLDEEVNGVHFTYTLNVMRKGLLGLDAFAKRNQDSTNA 372
QY 143 NHRSSGSVNTANHF-----NAMAQ--OGLT-----LGTMDYQIVAV 176

Db 373 STYSSSTASTIANKISSFWVSNMNIQVSVTGVSCKGLDVSTLLAANIGSYD----- 426
QY 177 EGFSSGSASI 187
Db 427 DGFPTPGSEKI 437

RESULT 50

G86797
Prophage p13 protein 09 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C:Accession: G86797

R:Polioin, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss

A:Reference number: AB6625; MUID:21235186; PMID:1137471

A:Accession: G86797

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-810 <STO>

A:Cross-references: GB:AE005176; PID:912724369; PIDN:AAK05481.1; GSPDB:GNO0146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: p1309

Query Match 15.18; Score 157.7; DB 2; Length 810;

Best Local Similarity 14.78; Pred. No. 45;

Matches 61; Conservative 32; Mismatches 60; Indels 263; Gaps 17;

QY 2 TTOPGTGVNN-----GYFYSY-----WNDHGGVTVTNGP 31
Db 400 TTPAPNTGWNISVPSLVKQYLMTKYWTYSDTTSETGYSVTYIAKDGNDCIAGKDG 459
QY 32 G-----GQFSVMNSNSGNFVGKGW----- 51
Db 460 GIKTTITFYAG-----STSGTIAPSSGMATVPVTAAGSYLMTKTVMAITDNTSETGYS 513
QY 52 -----QPGTK-----NKVIN-----FSG-----SYNPN 70
Db 514 VAKMGNNGATGPGCPGSGNDGPKIVSNTEPTTRFKGLTWKXIGMSDLTASDGTVIKIPNT 573
QY 71 NSYLSVYGMSRNPLIEYIVENFGTYNPSTGATKLGCVTSDCGSVDIYRTQVNPSPIT- 129
Db 574 EYYVNGTHM---VIVTFVNNFAES-----ITS-----KIDAKNLI 609
QY 130 -----GTATFYQYVSVRRNH-----RSSGSYNTANHFNAQAQG----- 163
Db 610 TDGEFVSTTNGPVVTST-----EIKDNHIAISKTDGTVNTKNDLAVDTEQGFAMKFTNN 664
QY 164 ----- 163
Db 665 TTGLTREASVNFQGVSTSDSNGNYAQLTPQGTKLSTDVPMNITRSSGVGTSGLRARIN 724
QY 164 -----LTGLTMDYQIYAVEGY-----FSSGS---ASITV 189
Db 725 NGVFYAKSDVITPSTAPNSIITIGTMSKFSKFSVSGFDTLGLLYSIGQLSVASVTV 780

Search completed: July 1, 2003, 11:49:09
Job time : 44 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2003, 11:47:35 ; Search time 11 Seconds

(without alignments)
716.409 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045
Sequence: 1 QTIQGTGYNGYFYSYWD.....YQIVAVEGYSSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt-40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1045	100.0	222	1 XYN2_TRIRE	P36217 trichoderma
2	990	94.7	190	1 XYN2_TRIFA	P48793 trichoderma
3	684.9	65.5	225	1 XYN1_EMENI	P55332 emeritella
4	676.9	64.8	225	1 XYNB_ASPAK	P48824 aspergillus
5	670.9	64.2	221	1 XYN2_EMENI	P55333 emeritella
6	664.9	63.6	225	1 XYN2_ASPNG	P55330 aspergillus
7	650.9	62.3	221	1 XYN1_COCCA	O06562 cochlidiolu
8	635.9	60.9	225	1 XYN1_THELA	O43097 thermomyces
9	614.9	58.8	227	1 XYN1_HUMIN	P55334 humicola in
10	600.4	57.5	335	1 XYNB_CELFI	P26515 streptomyc
11	577.5	55.3	644	1 XYN2_CELFI	P54865 cellulomona
12	572.7	54.8	233	1 XYN2_MAGCR	P55335 magnaporthe
13	568.3	54.4	197	1 XYN1_SCHCO	P35809 schizopyll
14	533.2	51.0	240	1 XYN1_STRLI	P26220 streptomyc
15	528.3	50.6	210	1 XYNB_BACST	P45705 bacillus st
16	506.2	48.4	213	1 XYNB_BACST	P18429 bacillus su
17	505.2	48.3	213	1 XYNB_BACCI	P09650 bacillus ci
18	466.6	44.7	228	1 XYNB_BACPU	P00694 bacillus pu
19	458.7	43.9	261	1 XYNB_CLOSA	P17137 clostridium
20	448.8	42.9	512	1 XYNB_CLOSR	P33558 clostridium
21	446.9	42.8	229	1 XYN1_TRIRE	P36218 trichoderma
22	434	41.5	211	1 XYN1_ASPNG	P55338 aspergillus
23	434	41.5	211	1 XYN1_ASPNG	P55339 aspergillus
24	432	41.3	211	1 XYN1_ASPNG	P55331 aspergillus
25	430.9	41.2	211	1 XYN3_ASPAK	P33557 aspergillus
26	410	39.2	954	1 XYNB_ROMFL	P29126 rumiilococu
27	392.5	37.6	802	1 XYNB_ROMFL	O53317 rumiilococu
28	316.1	30.2	607	1 XYNB_ROMPA	P29127 neocallimas
29	299.3	28.6	608	1 XYNB_ROMPA	P35811 fibrobacter
30	267.3	25.6	625	1 XYNB_ROMPA	O12667 pitomyces s
31	163.6	15.7	666	1 MUR2_ENTHR	P39046 enterococu
32	155.3	14.9	776	1 ISOA_PSEAY	P10342 pseudomonas
33	155.3	14.9	776	1 ISOA_PSESP	P26501 pseudomonas

34	153.3	14.7	604	1 AMYG_RHIOA	P07683 rhizopus or
35	151	14.4	987	1 YD94_METJA	O58789 methanococ
36	147.4	14.1	699	1 CH11_BACCI	P20533 bacillus ci
37	143.7	13.8	890	1 BCN5_CLOPE	P08696 clostridium
38	143.5	13.7	1196	1 AMYB_PAEPO	P21543 paenibacill
39	142.2	13.6	878	1 FIMD_ECOLI	P30130 escherichia
40	141.4	13.5	1341	1 VGS7_BPT2	P07067 bacterioph
41	140.6	13.5	969	1 SACH_STRSL	O5242 streptococ
42	140.1	13.4	366	1 OM3A_RHILV	O05811 rhizobium l
43	139.8	13.4	1953	1 BIGA_SALTY	P25927 salmonella
44	139.7	13.4	2334	1 WAPA_BACSU	O07833 bacillus su
45	139.4	13.3	941	1 GUN_BACSU	P19424 bacillus sp

ALIGNMENTS

RESULT 1
ID XYN2_TRIRE STANDARD: PRT: 222 AA.
AC P36217:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)
GN XYN2
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=C30;
RX MEDLINE=93103679; PubMed=1369024;
RA Toerrien A., Mach R.L., Messner R., Gonzalez R., Kalkkinen N.,
RA Harkki A., Kubicek C.P.;
RT "The two major xylanases from Trichoderma reesei: characterization of
RT both enzymes and genes";
RL Biotechnology 10:1461-1465(1992).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RC STRAIN=C30;
RX MEDLINE=94283373; PubMed=8013449;
RA Toerrien A., Harkki A., Rouvinen J.;
RT "Three-dimensional structure of endo-1,4-beta-xylanase II from
RT Trichoderma reesei: two conformational states in the active site";
RL EMBO J. 13:2493-2501(1994).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RC STRAIN=C30;
RX MEDLINE=95127663; PubMed=7827044;
RA Toerrien A., Rouvinen J.;
RT "Structural comparison of two major endo-1,4-xylanases from
RT Trichoderma reesei";
RL Biochemistry 34:847-856(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RC STRAIN=C30;
RX MEDLINE=96302263; PubMed=8755744;
RA Hvalby A., Toerrien A., Laitinen T., Rouvinen J.;
RT "Covalent binding of three epoxalyxosides to the active site of
RT endo-1,4-xylanase II from Trichoderma reesei";
RL Biochemistry 35:9617-9624(1996).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- PTM: THE N-TERMINUS IS BLOCKED.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation ;

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/> or send an email to license@ebi.ac.uk).

EMBL: X69573; CAA49293.1; -
PIR: S39154; S39154.
PDB: 1XVO: 08-AUG-95.
PDB: 1XYP: 08-AUG-95.
PDB: 1ENX: 08-AUG-95.
PDB: 1RED: 11-JAN-97.
PDB: 1REE: 11-JAN-97.
PDB: 1REF: 11-JAN-97.
InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRASE1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
Kxylan degradation; Hydrolase; Glycoprotein; Signal;
3D-structure.
FT SIGNAL 1 32
FT CHAIN 33 222 ENDO-1,4-BETA-XYLANASE 2.
FT ACT_SITE 118 118 NUCLEOPHILE.
FT CARBOHYD 209 209 PROTON DONOR.
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 222 AA; 24172 MW; 15F7032FACF9636F CRC64;

Query Match 100.0%; Score 1045; DB 1; Length 222;
Best Local Similarity 100.0%; Pred. No. 2,7e-39;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIPTGTGYNNGYYSYWNDDGCVTNTNGGQFVSVMNSGNGFVGKGMQPTKKKVI 60
DB 33 QTIPTGTGYNNGYYSYWNDDGCVTNTNGGQFVSVMNSGNGFVGKGMQPTKKKVI 92
QY 61 NFSGSYNPNNGSYLSYVGWSRNPLIEYIYENFGTYPNPGATKLGKLVSDGSYYDIYRT 120
DB 93 NFSGSYNPNNGSYLSYVGWSRNPLIEYIYENFGTYPNPGATKLGKLVSDGSYYDIYRT 152
QY 121 ORVNPSTIGATPTGYQWVSRRNRSSGSVNTANHFANMAOGLTGTMDYQIYAVGCF 180
DB 153 ORVNPSTIGATPTGYQWVSRRNRSSGSVNTANHFANMAOGLTGTMDYQIYAVGCF 212
QY 181 SSGSASITVS 190
DB 213 SSGSASITVS 222

RESULT 2
XYN1_TRIHA STANDARD; PRT; 190 AA.
ID XYN1_TRIHA
AC P48793;

DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylosidase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylo-
xylanohydrolase).
OS Trichoderma harzianum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Mitosporic Hyphomycetes; Trichoderma.
OX NCBI_TaxID=5544;
RN [1]
RP SEQUENCE.
RC STRAIN=ES8;
RA Yaguchi M., Roy C., Watson D.C., Rollin F., Tan L.U.L., Senior D.J.,
RA Sessler J.N.,
RT "The amino acid sequence of the 20 kD xylanase from Trichoderma
harzianum ES8".
RL (in) Visser J., Beldman G., Kusters-van Someren M.A.,
Voragen A.G.J. (eds.);

RL xylans and xylanases, pp.435-438, Elsevier, Amsterdam (1992).

(12)

RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).

RP Campbell R.L., Rose D.R., Wakarchuk W.W., To R.J., Sung W.,

RA Yaguchi M.,

RT "High-resolution structures of xylanases from B.circulans and

RT T.harzianum identify a new folding pattern and implications for the

RT atomic basis of the catalysis.";

RL (in) Suominen P., Reinkainen T. (eds.);

RL Trichoderma reesei cellulases and other hydrolases, pp.63-72,

RL Foundation for Biotechnical and Industrial Fermentation Research,

RL Helsinki (1993).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic

CC linkages in xylans.

CC -1- PATHWAY: Xylan degradation.

CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL

CC HYDROLASES)

PDB: 1XND: 20-DEC-94.

DR InterPro: IPR001137; GH_11.

DR Pfam: PF00457; Glyco_hydro_11; 1.

DR PRINTS: PR00911; GLHYDRASE1.

DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.

DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

Kxylan degradation; Hydrolase; Glycosidase; 3D-structure.

FT ACT_SITE 86 86 NUCLEOPHILE.

FT ACT_SITE 177 177 PROTON DONOR.

SEQUENCE 190 AA; 20703 MW; 6A0FAD1C3599C698 CRC64;

Query Match 94.7%; Score 990; DB 1; Length 190;
Best Local Similarity 94.2%; Pred. No. 5.1e-37;
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIPTGTGYNNGYYSYWNDDGCVTNTNGGQFVSVMNSGNGFVGKGMQPTKKKVI 60
DB 1 QTIPTGTGYNNGYYSYWNDDGCVTNTNGGQFVSVMNSGNGFVGKGMQPTKKKVI 60
QY 61 NFSGSYNPNNGSYLSYVGWSRNPLIEYIYENFGTYPNPGATKLGKLVSDGSYYDIYRT 120
DB 93 NFSGSYNPNNGSYLSYVGWSRNPLIEYIYENFGTYPNPGATKLGKLVSDGSYYDIYRT 120
QY 121 ORVNPSTIGATPTGYQWVSRRNRSSGSVNTANHFANMAOGLTGTMDYQIYAVGCF 180
DB 121 ORVNPSTIGATPTGYQWVSRRNRSSGSVNTANHFANMAOGLTGTMDYQIYAVGCF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 3
XYN1_EMENTI STANDARD; PRT; 225 AA.
ID XYN1_EMENTI
AC P55332; 000173;

DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylosidase 1 precursor (EC 3.2.1.8) (Xylanase 1)
DE (1,4-beta-D-xylo-xyloxyhydrolase 1).
OS Emeritella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emeritella.
OX NCBI_TaxID=5072;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96236210; PubMed=8787417;
RA Perez-Gonzalez J.A., de Graaf L.H., Visser J., Ramon D.;
RT "Molecular cloning and expression in Saccharomyces cerevisiae of two
RT Aspergillus nidulans xylanase genes.";
RL Appl. Environ. Microbiol. 62:2179-2182(1996).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL

CC HYDROLASES).

CC -----

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CC -----

CC EMBL: Z49892; CA90073.1; -

CC DR HSSP: P48793; 1XND.

CC DR InterPro: IPR001137; GH_11.

CC DR Pfam: PF00457; Glyco_hydro.11; 1.

CC DR PRINTS: PR00911; GLYHYDRLASE1.

CC DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.

CC DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

CC DR Xylan degradation; Hydrolase; Glycosidase; signal.

CC KW xylan degradation; Hydrolase; Glycosidase; signal.

CC FT SIGNAL 1 19 POTENTIAL.

CC FT CHAIN 20 225 ENDO-1,4-BETA-XYLANASE 1.

CC FT ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).

CC FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).

CC SQ SEQUENCE 225 AA: 24070 MW: 670527960207ECC CRC64;

CC -----

CC Query Match 65.5%; Score 684.9; DB 1; Length 225;

CC Best Local Similarity 66.1%; Pred. No. 1.5e-23;

CC Matches 121; Conservative 25; Mismatches 36; Indels 1; Gaps 1;

CC -----

CC QY 7 TGYNNGFYFYWMNDGHCVTYTNNGPGQFVSVMNSNGFVGKMGWPGTKNKVINFSGSY 66

CC Db 43 TGENNGYYYSFMTDGGGDVYTNNGNAGSYSEVMNSNGFVGKMGWPGSA-KDITYSGNF 101

CC QY 67 NPGNSYLSYVGSNRPLIEYIVENFGTYNPSTGATKLGCVYSDGSVDYDITRYQVNOP 126

CC Db 102 TPGNGYLSYVGSNRPLIEYIVESIGTYNPSSGQHRGTYSDDGFTDITATRYTNP 161

CC QY 127 SIIGTATFYQVMSVRNRHSSGVSNTANHFNAAGGLTGTDYQIVAVEGFSSGSSA 186

CC Db 162 SIEGTATFEQFMSVRQSKRTGTVTANHFNAAGLMRLGTHNYQIVAVEGFSSGSSA 221

CC QY 187 ITV 189

CC Db 222 ITV 224

CC -----

CC RESULT 4

CC XYNB_ASPAK STANDARD; PRT; 225 AA.

CC AC P48824;

CC DT 01-FEB-1996 (Rel. 33, Created)

CC DT 01-FEB-1996 (Rel. 33, Last sequence update)

CC DT 15-JUN-2002 (Rel. 41, Last annotation update)

CC DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)

CC DE (1,4-beta-D-xylan xylanohydrolase B).

CC GN XYNB.

CC OS Aspergillus awamori (var. kawachi).

CC OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

CC OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

CC OX NCBI_TaxID=40384;

CC RN 11

CC RP SEQUENCE FROM N.A.

CC RA STRAIN=IFO 4308;

CC RC Ito K.;

CC RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases

CC RL -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic

CC links in xylans.

CC CC -1- LINKAGES in xylans.

CC CC -1- PATHWAY: Xylan degradation.

CC CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL

CC HYDROLASES).

CC -----

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CC -----

CC DR EMBL: D38070; BAA07264.1; -

CC DR HSSP: P36217; 1XVO.

CC DR InterPro: IPR001137; GH_11.

CC DR Pfam: PF00457; Glyco_hydro.11; 1.

CC DR PRINTS: PR00911; GLYHYDRLASE1.

CC DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.

CC DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

CC DR Xylan degradation; Hydrolase; Glycosidase; signal.

CC FT SIGNAL 1 18 POTENTIAL.

CC FT CHAIN 19 225 ENDO-1,4-BETA-XYLANASE B.

CC FT ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).

CC FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).

CC SQ SEQUENCE 225 AA: 24146 MW: 54813048AF5C7115 CRC64;

CC -----

CC Query Match 64.8%; Score 676.9; DB 1; Length 225;

CC Best Local Similarity 66.1%; Pred. No. 3.3e-23;

CC Matches 121; Conservative 23; Mismatches 38; Indels 1; Gaps 1;

CC -----

CC QY 7 TGYNNGFYFYWMNDGHCVTYTNNGPGQFVSVMNSNGFVGKMGWPGTKNKVINFSGSY 66

CC Db 43 TGENNGYYYSFMTDGGGDVYTNNGNAGSYSEVMNSNGFVGKMGWPGSA-KDITYSGNF 101

CC QY 67 NPGNSYLSYVGSNRPLIEYIVENFGTYNPSTGATKLGCVYSDGSVDYDITRYQVNOP 126

CC Db 102 TPGNGYLSYVGSNRPLIEYIVESIGTYNPSSGQHRGTYSDDGFTDITATRYTNP 161

CC QY 127 SIIGTATFYQVMSVRNRHSSGVSNTANHFNAAGGLTGTDYQIVAVEGFSSGSSA 186

CC Db 162 SIEGTATFEQFMSVRQSKRTGTVTANHFNAAGLMRLGTHNYQIVAVEGFSSGSSA 221

CC QY 187 ITV 189

CC Db 222 ITI 224

CC -----

CC RESULT 5

CC XYN2_EMENTI STANDARD; PRT; 221 AA.

CC AC P55333; 000176;

CC DT 01-OCT-1996 (Rel. 34, Created)

CC DT 01-OCT-1996 (Rel. 34, Last sequence update)

CC DT 15-JUN-2002 (Rel. 41, Last annotation update)

CC DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)

CC DE (1,4-beta-D-xylan xylanohydrolase 2).

CC OS Emericella nidulans (Aspergillus nidulans).

CC OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

CC OC Eurotiales; Trichocomaceae; Emericella.

CC OX NCBI_TaxID=5072;

CC RN 11

CC RP SEQUENCE FROM N.A.

CC RX MEDLINE=96236210; PubMed=8787417;

CC RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;

CC RT "Molecular cloning and expression in *Saccharomyces cerevisiae* of two

CC RT Aspergillus nidulans xylanase genes.";

CC RL Appl. Environ. Microbiol. 62:2179-2182(1996).

CC CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic

CC links in xylans.

CC CC -1- LINKAGES in xylans.

CC CC -1- PATHWAY: Xylan degradation.

CC CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL

CC HYDROLASES).

CC -----

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CC -----

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CC -----
DR EMBL: Z49893; CA90074.1; -.
DR HSSP: P48793; 1XND.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Xylan degradation: Hydrolase; Glycosidase; signal.
KW Xylan degradation: Hydrolase; Glycosidase; signal.
FT SIGNAL 1 18
FT CHAIN 19 221
FT ACT_SITE 117 117
FT ACT_SITE 208 208
FT ACT_SITE 221 AA; 23517 MW; 42665E80DD9475 CRC64;
SO SEQUENCE

Query Match 64.2%; Score 670.9; DB 1; Length 221;
Best Local Similarity 65.8%; Pred. No. 5.9e-23;
Matches 121; Conservative 26; Mismatches 36; Indels 1; Gaps 1;

OY 7 TGYNNGFYSYWNDHGCVTYTNGPGQFYSVMSNSGNFVGKGMQPGTKRKVIINFGSGY 66
DB 39 TGTSGYYSFMTGGGCVTYTNGDGSYVEMTKVGNFVGKGMNPGS-SQTSISGSGF 97
OY 67 NPNNGSYLVYSGWGRNPLIEYIYENFGTYNPSGATKRLGEVTSDSGVYDIYTRQVRNOP 126
DB 98 TPGSGYLSYVGWTPNPLEIYIYVESYGDYNPAGTGHQGLTESDGYDIYTRATRENAP 157
OY 127 SIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTGTMDYQIYAVEGFSSGSAS 186
DB 158 SIETATFTQYWSVRQSKRTSGSVTTQNHFDANSQGLTGHNTQIYAVEGYOSSGSAS 217
OY 187 ITVS 190
DB 218 ITVS 221

RESULT 6
XYN2_ASPNG STANDARD: PRT: 225 AA.
AC P55330; Q12557;
DT 01-FEB-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase II precursor (EC 3.2.1.8) (Xylanase II)
DE (1,4-beta-D-xylan xylanohydrolase II).
GN XYNB.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 4066;
RA Ito K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation..
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC -----
DR EMBL: D38071; BAA07265.1; -.
DR HSSP: P09850; 1XNB.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
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DR PRINTS: PR00911; GLHYDRASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Xylan degradation: Hydrolase; Glycosidase; signal.
KW Xylan degradation: Hydrolase; Glycosidase; signal.
FT SIGNAL 1 18
FT PROPEP 19 37
FT CHAIN 38 225
FT ACT_SITE 121 121
FT ACT_SITE 212 212
FT ACT_SITE 225 AA; 24057 MW; C48BBB007AB2B8BD CRC64;
SO SEQUENCE

Query Match 63.6%; Score 664.9; DB 1; Length 225;
Best Local Similarity 65.6%; Pred. No. 1.1e-22;
Matches 120; Conservative 22; Mismatches 40; Indels 1; Gaps 1;

OY 7 TGYNNGFYSYWNDHGCVTYTNGPGQFYSVMSNSGNFVGKGMQPGTKRKVIINFGSGY 66
DB 43 TGNNGFYYSFMTGGGCVTYTNGDAGAYVEMSNVGNFVGKGMNPGSAD-ITYSCTF 101
OY 67 NPNNGSYLVYSGWGRNPLIEYIYENFGTYNPSGATKRLGEVTSDSGVYDIYTRQVRNOP 126
DB 102 TPGSGYLSYVGWTPNPLEIYIYVESYGDYNPAGTGHQGLTESDGYDIYTRATRENAP 161
OY 127 SIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTGTMDYQIYAVEGFSSGSAS 186
DB 162 SIETATFTQYWSVRQSKRTSGSVTTQNHFDANSQGLTGHNTQIYAVEGYOSSGSAS 221
OY 187 ITV 189
DB 222 ITV 224

RESULT 7
XYN1_COCCA STANDARD: PRT: 221 AA.
AC Q06562;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I)
DE (1,4-beta-D-xylan xylanohydrolase I).
GN XYL1.
OS Cochliobolus carbonum (Bipolaris zeicola).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5017;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Race 1 / Isolate SB111;
RA MEDLINE=94003417; PubMed=8400376;
RA Apel P.C., Panaccione D.G., Holden F.R., Walton J.D.;
RT "Cloning and targeted gene disruption of XYL1, a beta 1,4-xylanase
RT gene from the maize pathogen Cochliobolus carbonum."
RL Mol. Plant Microbe Interact. 6:467-473(1993).
RN [2]
RP PARTIAL SEQUENCE.
RA Holden F.R., Walton J.D.;
RT "Xylanases from the fungal maize pathogen Cochliobolus carbonum."
RL Physiol. Mol. Plant Pathol. 40:39-47(1992).
CC -1- FUNCTION: MAJOR XILAN-DEGRADING ENZYME. CONTRIBUTES TO THE
CC HYDROLYSIS OF ARABINOXYLAN, THE MAJOR COMPONENT OF MAIZE CELL-
CC WALLS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PM: THE N-TERMINUS IS BLOCKED.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC linkages in xylans.
CC -1- PATHWAY: xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X76047; CAA53632.1; -
CC HSSP: Q43097; 1XNA.
CC InterPro: IPR001137; GH_11.
CC Pfam: PF00457; Glyco_hydro.11; 1.
CC PRINTS: PR00911; GLHYDRASE1.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC DR Xylan degradation; Hydrolase; Glycosidase; signal.
CC KW SIGNAL 1 19
CC FT CHAIN 20 227
FT ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 227 AA; 25601 MW; 5C2FE6ADCEADAIF CRC64;

Query Match 58.8%; Score 614.9; DB 1; Length 227;
Best Local Similarity 58.8%; Pred. No. 1.7e-20;
Matches 107; Conservative 26; Mismatches 48; Indels 1; Gaps 1;

QY 8 GYNNGYFYSYNDGHCVTYTNPGCGQFSVMNSNGNFVCGKMGWPGTKKNKYNFSGSYN 67
DB 4 GHHNHYFFYSWSDGGGOVYTNLEGRYOVRRNRNGNFVCGKMGWPGT -GRTINNGYFN 102
QY 68 PNGNSYLVYSGWSRNPLEYIVENFGTYNPSTGATKGEVTSQGSVDYRTQVNPSPS 127
DB 103 POGNGLYAVGTRNPLVEYIVESYTYNPGSQOYGTYYTDDQYDFVSTRYNOPS 162
QY 128 IIGTATFYQVYSVRNRHSSGVNTANFNHMAAOGLTGTMDYQIVAVEGYFSSGSASI 187
DB 163 IDGTRTFQOYWSIRKNRVGSGVMNQHNFMNAQOHGMPGLGHYYQVAVTEGYSGSGESDI 222
QY 188 TV 189
DB 223 YV 224

RESULT 10

XYNB_STRLI STANDARD; PRT; 335 AA.
ID XYNB_STRLI STANDARD; PRT; 335 AA.
AC P26515;
DT 01-AUG-1992 (Rel. 23, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (xylanase B)
DE (1,4-beta-D-xylan xylanohydrolase B).
GN XLNB.
OS Streptomyces lividans.
OS Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
CC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 42-72.
RP STRAIN=66 / 1326;
RC MEDLINE=92077439; PubMed=1743521;
RA Shreck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
RT "Sequences of three genes specifying xylanases in Streptomyces
RT lividans.";
RL Gene 107:75-82(1991).
RP [2]
RP REVISIONS TO 29-32 AND 252-307.
RC STRAIN=66 / 1326;

RX MEDLINE=95189090; PubMed=7533741;
RA Shreck F., Biely P., Morosoli R., Kluepfel D.;
RT "Analysis of DNA flanking the xln locus of Streptomyces lividans
RT reveals genes encoding acetyl xylan esterase and the RNA component of
RT ribonuclease P.";
RL Gene 153:105-109(1995).
RN [3]
RN REVISION TO 225.
RP Shreck F.;
RA Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CONTRIBUTES TO HYDROLYSE HEMICELLULOSE, THE MAJOR
CC COMPONENT OF PLANT CELL-WALLS. XLNA AND XLNB SEEM TO ACT
CC SEQUENTIALLY ON THE SUBSTRATE TO YIELD XYLOBIOSIDE AND XYLOSE
CC AS CARBON SOURCES.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC -----
CC EMBL: M64552; AAC06114.2; -
CC HSSP: P09850; 1XNB.
CC InterPro: IPR001137; GH_11.
CC Pfam: PF00457; Glyco_hydro.11; 1.
CC PRINTS: PR00911; GLHYDRASE1.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC DR Xylan degradation; Hydrolase; Glycosidase; signal.
CC KW SIGNAL 1 41
CC FT CHAIN 42 335
FT DOMAIN 42 230
FT DOMAIN 231 249
FT DOMAIN 250 335
FT DOMAIN 128 128 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 218 218 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 335 AA; 35575 MW; 513B1458BF8FCF CRC64;

Query Match 57.5%; Score 600.4; DB 1; Length 335;
Best Local Similarity 55.1%; Pred. No. 1.5e-19;
Matches 109; Conservative 32; Mismatches 41; Indels 16; Gaps 5;

QY 5 PGT-----GYNNGYFYSYNDGHCVTYTNPGCGQFSVMNSNGNFVCGKMGW 52
DB 36 PGTAQADIVYTTNDEGTRNGYVFWTDSQCTVSMNMGSGQYSTSRKRNQNFPAAGGWA 95
QY 53 PGTNNKYNFSGSYNPNNGNSLYVSGWSRNPLEYIVENFGTYNPSTGATKGLGEVTS 112
DB 96 NGR-RTVQYSGSPNPGNAVLYGWSNPLVEYIVDMNGTYRP-TGEYK-CTVYSDG 152
QY 113 SVYDIYTORVNOISITGATFYQVYSVRNRHSSGVNTANFNHMAAOGLTGTMD-Y 171
DB 153 GTYDIYTRVKNKSPVSTFTPDQYVSVSRKRTGRTTGNHFDAMRAGMPLGNFSY 212
QY 172 QIVAVEGYFSSGSASITV 189
DB 213 MIMATBEYQSSGSSINAV 230

RESULT 11

XYND_CELFI STANDARD; PRT; 644 AA.
ID XYND_CELFI STANDARD; PRT; 644 AA.
AC P54865;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase D precursor (EC 3.2.1.8) (Xylanase D) (XYLD).
 GN XYND.
 OS Cellulomonas flm.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Micrococciaceae; Cellulomonadaceae; Cellulomonas.
 OX NCBI_TaxID=1708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=221;
 RX MEDLINE=94224155; PubMed=8170399;
 RA Millward-Sadler S.J., Poole D.M., Henriessat B., Hazlewood G.P.,
 RA Clarke J.H., Gilbert H.J.;
 RT "Evidence for a general role for high-affinity non-catalytic
 RT cellulose binding domains in microbial plant cell wall hydrolases.";
 RL Mol. Microbiol. 11:375-382(1994).
 CC -1- FUNCTION: ENDOACTING XYLANASE WHICH DISPLAYS NO DETECTABLE
 CC ACTIVITY AGAINST POLYSACCHARIDES OTHER THAN XYLAN. HYDROLYSES
 CC GLUCOSIDIC BONDS WITH RETENTION OF ANOMERIC CONFIGURATION.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X76729; CA54145.1; -
 CC HSSP: P09850; 1XNB.
 DR InterPro: IPR001919; Bac_cellose-bind.
 DR InterPro: IPR001137; GH_11.
 DR InterPro: IPR002509; Polysac_deacet.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR Pfam: PF00553; CBM_2; 2.
 DR Pfam: PF01522; Polysac_deacet; 1.
 DR PRINTS: PR00911; GLHYDRASE1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Hydrolase; Glycosidase; Signal; Repeat.
 FT SIGNAL 1 43 POTENTIAL.
 FT CHAIN 44 644 ENDO-1,4-BETA-XYLANASE D.
 FT DOMAIN 44 230 CATALYTIC.
 FT DOMAIN 231 245 LINKER ("HINGE") (GLY-RICH BOX).
 FT DOMAIN 246 644 2 X 88 AA APPROXIMATE CBD-LIKE REPEATS.
 FT REPEAT 246 333 1.
 FT REPEAT 333 644 2.
 FT DOMAIN 337 350 LINKER ("HINGE") (PRO-THR BOX).
 FT SIMILAR 351 547 SOME TO R. MELLLOTT NODB.
 FT DOMAIN 548 556 LINKER ("HINGE") (GLY-RICH BOX).
 FT DOMAIN 231 238 POLY-GLY.
 FT DOMAIN 241 245 POLY-GLY.
 FT DOMAIN 548 558 POLY-GLY.
 FT ACT_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 216 216 PROTON DONOR (BY SIMILARITY).
 FT SEQUENCE 644 AA; 66581 MW; 568045CCE0E1820 CRC64;
 SO
 Query Match 55.3%; Score 577.5; DB 1; Length 644;
 Best Local Similarity 55.7%; Pred. No. 5e-18;
 Matches 103; Conservative 39; Mismatches 38; Indels 5; Gaps 4;

OY 7 TGYNNGYVSTYWNDSHGCVTYTNGGQFVSVMNSNGNFVGKGMQPTKXKVI NFGSSY 66
 DB 49 TGTHTGYSTFWTDSPGVSMDLNGGCGYT-RMSNTGKFNFAKGMSTGR-KTVSYSGOF 106
 OY 67 NPNNGSYLVYSGMSNPLILEYIVENFGTYNPGTATLGTEVTSYGSDYDIYRQORVNP 126
 DB 107 NPSRNVLTLLTGWTSPLVEYIVLSEYIVLSEYIVLSEYIVLSEYIVLSEYIVLSEYIV 164
 OY 127 SIIG-TATFYQVSVRRNRHSSGVSNTANHNANAOGLTLGTDYOIVAEGYFSSGSA 185
 DB 165 SIEGDSSTFYQVSVRRNRHSSGVSNTANHNANAOGLTLGTDYOIVAEGYFSSGSA 224
 OY 186 STVS 190
 DB 225 STVS 229
 RESULT 12
 XYN2_MAGGR STANDARD; PRT; 233 AA.
 ID XYN2_MAGGR
 AC P55335; Q01171;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase 22 precursor (EC 3.2.1.8) (Xylanase 22)
 DE (1,4-beta-D-xylan xylanhidrolase 22).
 GN XYN22.
 OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes; incertae sedis; Magnaporthaceae; Magnaporthe.
 OX NCBI_TaxID=148305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KEN60-19;
 RX MEDLINE=96172742; PubMed=8589407;
 RA Wu S.C., Kaufman S., Darvill A.G., Albersheim P.;
 RT "Purification, cloning and characterization of two xylanases from
 RT Magnaporthe grisea, the rice blast fungus";
 RL Mol. Plant Microbe Interact. 8:506-514(1995).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L37529; AAC41683.1; -
 CC HSSP: O43097; 1YNA.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRASE1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation; Hydrolase; Signal.
 FT SIGNAL 1 39 POTENTIAL.
 FT CHAIN 40 233 ENDO-1,4-BETA-XYLANASE 22.
 FT ACT_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 217 217 PROTON DONOR (BY SIMILARITY).
 FT SEQUENCE 233 AA; 25491 MW; 40096383F581F98 CRC64;
 SO
 Query Match 54.8%; Score 572.7; DB 1; Length 233;
 Best Local Similarity 51.8%; Pred. No. 1.3e-18;
 Matches 99; Conservative 35; Mismatches 54; Indels 3; Gaps 2;

Db 159 ESTRVNOPSIEGRTFOQYWAIRQKRNKSGTNTGFEQAMERAGKRMGNHNMIVATGEG 218
QY 179 YFSSGSASITV 189
Db 219 YRSAGNSNINV 229

RESULT 13
XVNA_SCHCO STANDARD: PRT: 197 AA.

AC P35809;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase A (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan
Xylanohydrolase A).
GN XYNA.
OS Schizophyllum commune (Bracket fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Schizophyllaceae; Schizophyllum.
OX NCBI_TaxID=5334;
RN [1]
RP SEQUENCE.
RC STRAIN-ATCC 38548 / Delmar;
RA Yaguchi M., Roy C., Ujile M., Watson D.C., Wakarchuk W.;
RL (in) Visser J., Beidman G., Kusters-van Someren M.A.,
RL Voragen A.G.J. (eds.);
RL Xylans and xylanases, pp.149-154, Elsevier, Amsterdam (1992).
RN [2]
RP SEQUENCE, AND DISULFIDE BONDS.
RC STRAIN-ATCC 38548 / Delmar;
RX MEDLINE=94063044; PubMed=8243636;
RA Oku T., Roy C., Watson D.C., Wakarchuk W., Campbell R., Yaguchi M.,
RT Jurasek L., Palce M.G.;
RT "Amino acid sequence and thermostability of xylanase A from
Schizophyllum commune";
RT FEBS Lett. 334:296-300(1993).
RN [3]
RP PARTIAL SEQUENCE, AND ACTIVE SITE GLU-87.
RC STRAIN-ATCC 38548 / Delmar;
RX MEDLINE=94155888; PubMed=7906649;
RA Bray M.R., Clarke A.J.;
RT "Identification of a glutamate residue at the active site of xylanase
A from Schizophyllum commune";
RT Eur. J. Biochem. 219:821-827(1994).
CC -1- FUNCTION: HYDROLYSES XYLANS INTO XYLOBIOSE AND XYLOSE. THIS
CC XYLANASE HAS A VERY BROAD PH ACTIVITY.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR PIR: S38973; S38973.
DR PIR: A44597; A44597.
DR HSSP: O43097; LYNA.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW xylan degradation; Hydrolase; Glycosidase.
FT ACT_SITE 87 87 NUCLEOPHILE (PROBABLE).
FT ACT_SITE 184 184 PROTON DONOR (BY SIMILARITY).
FT DISULFID 111 160
SQ SEQUENCE 197 AA: 20978 MW: 4268074E67C1FBE9 CRC64;

Query Match 54.4%; Score 568.3; DB 1; Length 197;
Best local Similarity 55.0%; Pred. No. 1,4e-18;
Matches 105; Conservative 34; Mismatches 45; Indels 7; Gaps 3;

QY 7 TGYNGYFYSYMNDGHGVYTINGPGQPSVNMN-NSGNFVGKGMQPTKKNKVINFGSGS 65

Db 7 TGTDDGYIYSMTWDGADGATYQNNGGSGTYLTMSSGNNGMLYGGKGNPCAAARSISYST 66
QY 66 YNPNGNSYLSVIGWASNPLEIYVENFCTYNDPSTGATKLGVTSDGSYDIYRQRVNQ 125
Db 67 YOPNGNSYLSVIGWTRSSLSLEYIYESGYSYPSSAASHKSGVTCNGATYDLSTWRVNA 126
QY 126 PSTIGTATFYQWASVRNHRIS-----SGSVNTHNHNMAAQGLTLGT-NDYQIVAVEGY 179
Db 127 PSTDGTQTDFQWNSVNPKKAPGGSISGTVDVOCHPDAMKGLAMNLGSEHNQIVATGEG 186
QY 180 FSSGSASITVS 190
Db 187 QSSGTAITIVT 197

RESULT 14
XVNC_STRLI STANDARD: PRT: 240 AA.

AC P26220;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8) (Xylanase C)
GN XLNC.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-80.
RC STRAIN-66 / 1326;
RX MEDLINE=92077439; PubMed=1743521;
RA Sharack F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
RT "Sequences of three genes specifying xylanases in Streptomyces
RT lividans";
RT Gene 107:75-82(1991).
CC -1- FUNCTION: CONTRIBUTES TO HYDROLYSE HEMICELLULOSE, THE MAJOR
CC COMPONENT OF PLANT CELL-WALLS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M64553; AAA26836.1; -
DR EMBL: A25307; CAA01768.1; -
DR PIR: JS0591; JS0591.
DR HSSP: P09850; IXNB.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 49
FT CHAIN 50 240 ENDO-1,4-BETA-XYLANASE C.
FT ACT_SITE 134 134 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 226 226 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 240 AA: 25673 MW: FC663415780142CA CRC64;

Query Match 51.0%; Score 533.2; DB 1; Length 240;
Best local Similarity 50.5%; Pred. No. 7.1e-17;

	Matches	101: Conservative	31: Mismatches	50: Indels	18: Gaps	6
QY	5	PGTGY-----	NNGTFYSYNNDDHGCTTTNNPGGCGSYVMNNSGNTVVGCKGWGP			53
Db	44	PGTAAATTTT	NGTGTGMYTSFPTDDGGSVMTLNGGSGYSTQMTNCGNTVVGKRWGT			103
QY	54	GTRKNVIFSGSYNPGNSLSYVQMSRNP	LEYIVENFNGYTNPESTGATKLGEEVSDGS			113
Db	104	GDGN--VAVNGVFENVGNGGGLGYMTS	NPLEYEIVTDWMSYRP-TGYIK-CTVSSDDG			159
QY	114	VYDIYTRQVNOPSLIGATFYQVYSRRNRHSSGS	--VNTAHFNMAAQGLTIGTMD-			170
Db	160	TYDIYQTRVYAPSVEGTKTFEQQYSVSROS	KVTSKSGTITGNHFDAMARACMNMGOFRY			219
QY	171	YOIVAVEGYFSGSASITVS	190			
Db	220	YIMATFEGYSSGSSNITVS	239			

RESULT 15	
XYNA_BACST	STANDARD: PRT: 210 AA.
ID XYNA_BACST	
AC P45705:	
DT 01-NOV-1995 (Rel. 32, Created)	
DT 15-JUL-1998 (Rel. 36, Last sequence update)	
DT 15-JUN-2002 (Rel. 41, Last annotation update)	
DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)	
DE (1,4-beta-D-xylan xylanohydrolase A).	
GN XYNA.	
OS Bacillus stearothermophilus.	
OC Bacteria; Firmicutes; Bacillales; Geobacillus.	
OX NCBI_TaxID=1422;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN-NO. 236;	
RC Cho S., Choi Y.;	
RA "Nucleotide sequence analysis of an endo-xylanase gene (xyna) from	
RT Bacillus stearothermophilus.";	
RL J. Microbiol. Biotechnol. 5:117-124(1995).	
RN [2]	
RP REVISIONS.	
RC STRAIN-NO. 236;	
RC Cho S., Choi Y.;	
RA submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.	
RL -1- CATALYTIC ACTIVITY: Endohydrolays of 1,4-beta-D-xylosidic	
CC linkages in xylans.	
CC -1- PATHWAY: Xylan degradation.	
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL	
CC HYDROLASES).	
CC -----	
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CC -----	
DR EMBL: U15985; AAB72117.1; .	
DR HSSP: P09850; 1XNB.	
DR InterPro: IPR001137; GH_11.	
DR Pfam: PF00457; Glyco_hydro_11; 1.	
DR PRINTS: PR00911; GLHYDRASE11.	
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.	
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.	
KW xylan degradation; Hydrolase; Glycosidase; Signal.	
FT SIGNAL 1 19	POTENTIAL.
FT CHAIN 20 210	ENDO-1,4-BETA-XYLANASE A.
FT ACT_SITE 104 104	NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 197 197	PROTON DONOR (BY SIMILARITY).
SO SEQUENCE 210 AA: 23221 MW: 3190CF74C34AAB45 CR664;	
Query Match	50.6%; Score 528.3; DB 1; Length 210;

ID	XYNA_BACSU	STANDARD:	PRT:	213 AA.
AC	18429;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (xylanase A)			
DE	(1,4-beta-D-xylan xylanohydrolase A).			
GN	XYNA.			
OS	Bacillus subtilis.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1423;			
RP	SEQUENCE FROM N.A.			
RA	Palace M.G., Boudonnais R., Destrochers M., Juraske L., Yaguchi M.			
RT	"A xylanase gene from Bacillus subtilis: nucleotide sequence and			
RT	comparison with B. pumilus gene."			
RL	Arch. Microbiol. 144:201-206(1986).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Lapidus A., Galleron N., Sorokin A., Ehlich S.D.			
RT	"Sequence analysis of the Bacillus subtilis chromosome region between			
RT	the tect and ocbAB loci cloned in a yeast artificial chromosome."			
RL	Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=168;			
RX	MEBLIN=98044033; PubMed=9384377;			
RA	Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,			
RA	Azevedo V., Bertero M.C., Bessieres P., Bolotin A., Borchert S.,			
RA	Borris R., Bousnier L., Brans A., Braun M., Brignell S.C., Bron S.,			
RA	Brouillet S., Brusci C.V., Caldwell B., Capuano V., Carter N.M.,			
RA	Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,			
RA	Denizlot F., Devine K.M., Dusterhoft A., Ehlich S.D., Emerson P.T.,			
RA	Enrian K.D., Errington J., Fabre C.C., Ferrari E., Foulger D.,			
RA	Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,			
RA	Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,			
RA	Giuseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Hentut A.,			
RA	Hilbert R., Holzapfel S., Hosono S., Hullo M.F., Itaya M., Jones L.,			
RA	Joris B., Katamata D., Kasahara Y., Klier-Blanchard M., Klein C.,			
RA	Kobayashi Y., Koeller P., Konungstein G., Krogh S., Kumano M.,			
RA	Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,			
RA	Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,			
RA	Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,			
RA	Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,			
RA	Patro V., Pohl T.M., Portetelle D., Potworlik S., Prescott A.M.,			
RA	Presseau E., Pujic P., Purnelle D., Rapoport G., Rey M., Reynolds S.,			
RA	Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,			
RA	Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,			
RA	Sekiguchi J., Sekowski A., Seror S.J., Serron P., Shin B.S., Soldo B.,			
RA	Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,			
RA	Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,			

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzengger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
RT *subtilis*.";
RN Nature 390:249-256(1997).
RN (4)
RP MUTAGENESIS.
RA Makarchuk W., Method N., Lanthier P., Sung W., Seligy V., Yaguchi M.,
RA To R., Campbell R., Rose D., Kusters-van Someren M.A.,
RL (In) Visser J., Belman G., Kusters-van Someren M.A.,
RL Voragen A.G.J. (eds.);
RL Ylans and xylanases, pp.439-442, Elsevier, Amsterdam (1992).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC -----
DR EMBL: M36648; AAA22897.1; -
DR EMBL: AF027868; AAB84458.1; -
DR EMBL: 289114; CAB3776.1; -
DR PIR: S3157; S3157.
DR HSSP: P09850; 1XNB.
DR Subtilist: BG10808; xyna.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM xylan degradation; Hydrolase; Glycosidase; Signal; Complete proteome.
FT CHAIN 1 29 213
FT ACT_SITE 106 106 ENDO-1,4-BETA-XYLANASE A.
FT ACT_SITE 200 200 PROTON DONOR (BY SIMILARITY).
FT MUTAGEN 106 106 E->S: DRASTICALLY REDUCED ACTIVITY.
FT MUTAGEN 200 200 E->S: DRASTICALLY REDUCED ACTIVITY.
SQ SEQUENCE 213 AA; 23345 MW; 20CBA35238CC0564.CRC64;
Query Match 48.4%; Score 506.2; DB 1; Length 213;
Best Local Similarity 53.8%; Pred. No. 8, 6e-16;
Matches 98; Conservative 29; Mismatches 47; Indels 8; Gaps 6;
OY 14 FYSYWNHGHTVYTNPGGQFSVNMNSGNFVGKGMQPGTKNKVINF-SCSYNPNGNS 72
DB 33 YWQNMWDGCGIYVNAVNGSGNYSVNMNSGNFVGKGMQPGTKNKVINF-SCSYNPNGNS 92
OY 73 YLSYVGMSRNPLEYIYVENFGTYNPSTGATKLGKTYSDGSYDYDTRORVNPSTIG-T 131
DB 93 YLTLYGMRSPLEYIYVVDVSMGTYRP-TGTYK-GTVKSDGTYDYDITTRVNAPIIDGDR 150
OY 132 AFYQYQWYVRNRHRSQS---VNTANHFNAQAQGLTGT-MDYQIVANEGFFSSGASAI 187
DB 151 TTFQYQWYVRNRHRSQS---VNTANHFNAQAQGLTGT-MDYQIVANEGFFSSGASAI 210
OY 188 TV 189
DB 211 TV 212
RESULT 17
XYNA_BACCI STANDARD: PRT: 213 AA.
AC P09850;

DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (xylanase) (1,4-beta-D-
DE xylan xylanohydrolase).
GN XLNA.
OS *Bacillus* circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
OX NCBI_TaxID=1397;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=88303346; PubMed=3405767;
RA Yang R.C.A., Mackenzie C.R., Narang S.A.;
RT "Nucleotide sequence of a *Bacillus* circulans xylanase gene."
RN Nucleic Acids Res. 16:7187-7187(1988).
RN (2)
RX X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS), AND MUTAGENESIS.
RX MEDLINE=94290322; PubMed=8019418;
RA Makarchuk W.M., Campbell R.L., Sung W.L., Davoodi J., Yaguchi M.;
RT "Mutational and crystallographic analyses of the active site residues
RL of the *Bacillus* circulans xylanase."
RN Protein Sci. 3:467-475(1994).
RN (3)
RP STRUCTURE BY NMR.
RX MEDLINE=96322313; PubMed=8756457;
RA McIntosh L.P., Hand G., Johnson P.E., Joshi M.D., Koerner M.,
RA Plesniak L.A., Ziser L., Makarchuk W.M., Withers S.G.;
RT "The pKa of the general acid/base carboxyl group of a glycosidase
RT xylanase."
RL Biochemistry 35:9958-9966(1996).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC -----
DR EMBL: X07723; CAA30553.1; -
DR PIR: S01734; S01734.
DR PDB: 1BCX; 15-OCT-94.
DR PDB: 1XNB; 20-DEC-94.
DR PDB: 1XNC; 20-DEC-94.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM xylan degradation; Hydrolase; Glycosidase; Signal; 3D-structure.
FT CHAIN 1 29 213
FT ACT_SITE 106 106 ENDO-1,4-BETA-XYLANASE.
FT ACT_SITE 200 200 PROTON DONOR.
SQ SEQUENCE 213 AA; 23359 MW; 4BA0A35238CC00135 CRC64;
Query Match 48.3%; Score 505.2; DB 1; Length 213;
Best Local Similarity 53.8%; Pred. No. 9, 5e-16;
Matches 98; Conservative 28; Mismatches 48; Indels 8; Gaps 6;
OY 14 FYSYWNHGHTVYTNPGGQFSVNMNSGNFVGKGMQPGTKNKVINF-SCSYNPNGNS 72
DB 33 YWQNMWDGCGIYVNAVNGSGNYSVNMNSGNFVGKGMQPGTKNKVINF-SCSYNPNGNS 92
OY 73 YLSYVGMSRNPLEYIYVENFGTYNPSTGATKLGKTYSDGSYDYDTRORVNPSTIG-T 131
DB 93 YLTLYGMRSPLEYIYVVDVSMGTYRP-TGTYK-GTVKSDGTYDYDITTRVNAPIIDGDR 150


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OY 132 ATFOYMSVRNRHRRSSG---VNTANHNMAAOGLTGT-MDYOIVAVEGYFSSGSASI 187
DB 131 TTFOTYMSVRROSKRTGTSNATITTFNNHNAMKSHGMNLSGMNAYVMATEGYOSSGSSNV 210
OY 188 TV 189
DB 211 TV 212

RESULT 18
XNA_BACPU STANDARD: PRT; 228 AA.
ID XNA_BACPU STANDARD: PRT; 228 AA.
AC P00694;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)
DE (1,4-beta-D-xylan xylanohydrolase A).
GN XNA.
OS Bacillus pumilus (Bacillus mesentericus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1408;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-1P0;
RA Fukusaki E., Panbanged W., Shimmyo A., Okada H.;
RT "The complete nucleotide sequence of the xylanase gene (xyna) of
RT Bacillus pumilus.";
RL FEBS Lett. 171:197-201(1984).
RN [2]
RN REVISION TO 103.
RA Uraibe I.;
RN Submitted (FEB-1991) to the EMBL/Genbank/DBJ databases.
RN [3]
RN MUTAGENESIS, AND ACTIVE SITES.
RX MEDLINE=93075064; PubMed=1359880;
RX Ko E.P., Akatsuka H., Moriyama H., Shimmyo A., Hata Y., Katsube Y.,
RA Uraibe I., Okada H.;
RT "Site-directed mutagenesis at aspartate and glutamate residues of
RT xylanase from Bacillus pumilus.";
RL Biochem. J. 288:117-121(1992).
RN [4]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=93075064; PubMed=1359880;
RA Hata Y., Moriyama H., Shimmyo A., Okada H., Katsube Y.;
RL Unpublished results, cited by:
RL Ko E.P., Akatsuka H., Moriyama H., Shimmyo A., Hata Y., Katsube Y.,
RL Uraibe I., Okada H.;
RL Biochem. J. 288:117-121(1992).
CC -! CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -! PATHWAY: xylan degradation.
CC -! SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC -----
CC EMBL: X00660; CAA25278.1; -
CC PIR: A00848; WMBSPX.
CC HSSP: P09850; 1XNB.
CC InterPro: IPR001137; GH_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC PRINTS: PR00911; GLHYDRASE11.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW xylan degradation; Hydrolase; Glycosidase; signal.

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FT SIGNAL 1 27
FT CHAIN 28 228 ENDO-1,4-BETA-XYLANASE A.
FT ACT_SITE 120 120 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 209 209 PROTON DONOR (BY SIMILARITY).
FT MUTAGEN 120 120 E->S: LOSS OF ACTIVITY.
FT MUTAGEN 209 209 E->D: LOSS OF ACTIVITY.
SQ SEQUENCE 228 AA; 25491 MW; 32EF9833E7B5E503 CRC64;

Query Match 44.7%; Score 466.6; DB 1; Length 228;
Best Local Similarity 50.3%; Pred. No. 5.2e-14;
Matches 95; Conservative 25; Mismatches 35; Indels 14; Gaps 5;

OY 8 GYNNGCFYSYWNDDGVTYTNPCGOFSPVMSNSGNFGGK-----WQGTNKK 58
DB 36 GNHSGDYDELMKD-YGNISMTLLNNGAFSAGHNNTGNLFRKKFDSRTTHQLG--NI 92
OY 59 VINFSGSYNPNQNSYLSVYSGSRNLEIYIYVENEGTYNPSTGATKLGVTSDGSVDIY 118
DB 93 SINYNASENPGNSYLCVYGTQSPLEIYIYDWSGTYRP-TGAVK-GSFVADGGTVDIY 150
OY 119 RTQRYNOPSIIIGTAFYQYMSVRNRHRRSSGVSNTANHNMAAOGLTGTMDYOIVAVEG 178
DB 151 ETRRYNOPSIIIGTAFYQYMSVRNRHRRSSGVSNTANHNMAAOGLTGTMDYOIVAVEG 210
OY 179 YFSSGSAS 187
DB 211 YOSSGSANV 219

RESULT 19
XNA_CLOSA STANDARD: PRT; 261 AA.
ID XNA_CLOSA STANDARD: PRT; 261 AA.
AC P17137;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-
DE xylan xylanohydrolase).
GN XNB.
OS Clostridium saccharobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=169679;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-P262;
RX MEDLINE=90245673; PubMed=2336398;
RX Zappe H., Jones W.A., Woods D.R.;
RT "Nucleotide sequence of a Clostridium acetobutylicum P262 xylanase
RT gene (xynB).";
RL Nucleic Acids Res. 18:2179-2179(1990).
CC -! CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -! PATHWAY: xylan degradation.
CC -! SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -! CAUTION: Was originally thought to originate from
CC C.acetobutylicum.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M31726; AAA23287.1; -
CC PIR: S12745; S12745.
CC HSSP: P36217; 1XYO.
CC InterPro: IPR001137; GH_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC PRINTS: PR00911; GLHYDRASE11.

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DR PROSITE: PS00776; GLYCOSYL-HYDROL.FIL.1; 1.
DR PROSITE: PS00777; GLYCOSYL-HYDROL.FIL.2; 1.
KW Xylan degradation: Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 28
FT CHAIN 29 261 ENDO-1,4-BETA-XYLANASE.
FT ACT_SITE 152 152 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 242 242 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 261 AA: 29032 MW: 339C36146F6D14AE CRC64;

Query Match 43.9%; Score 458.7; DB 1; Length 261;
Best Local Similarity 47.1%; Pred. No. 1.5e-13;
Matches 89; Conservative 27; Mismatches 60; Indels 13; Gaps 4;

OY GYNNGEFSYNNNDGCGVTYINGPGCGGSVMKNSGNTVGGK-----WPGTKNK 58
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 68 GYNGGYDELKMD-YGNTSMPLKNKGASCOMSNIGNALFRGKKFNDDTQYKOLG--NI 124
OY 59 VINFSGSNPNNGSYLSYSGWRNRLIEIYIYENGTNPSTGATKLGKVTSDGSVDYI 118
Db | : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 125 SVNYCNCNPQGNSTLCYCYGTTSSPLVERIYDVSNGSRPPGGTSK-GTIYDGSITLY 183
OY 119 RTQRYNPDSITIGTATFYQYWSVRNRNRSSGSVNTANHPNMAAQGLLTGNDQYIYAVEG 178
Db | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 184 ETRTRNSIGNGTTFKQYWSVRRKTRPSGTISVSKHPAAMESKMPGKMHETAFNIEG 243
OY 179 YFSSSSASI 187
Db | | | | | :
OY 244 YOSSGKADV 252

RESULT 20
XYNA_CLOSR
ID XYNA_CLOSR STANDARD; PRT: 512 AA.
AC P33558;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase A precursor (BC 3.2.1.8) (Xylanase A)
DE (1,4-beta-D-xylan xylanohydrolase A).
GN XYNA.
OS Clostridium stercoararium.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1510;
RX MEDLINE=93214115; PubMed=7763496;
RA Sakka K., Kojima Y., Kondo T., Karita S.-I., Omiya K., Shimada K.;
RT "Nucleotide sequence of the Clostridium stercoararium xyna gene
RT encoding xylanase A: Identification of catalytic and cellulose
RT binding domains.";
RL Biosci. Biotechnol. Biochem. 57:273-277(1993).
RP REVISIONS.
RC STRAIN=F-9;
RA Sakka K.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolasts of 1,4-beta-D-xylosidic
CC linkages in xyans.
CC -1- PATHWAY: Xylan degradation.
CC -1- MISCELLANEOUS: HAS THERMOPHILIC PROPERTY (MAXIMUM ACTIVITY AT 70
CC DEGREE CELSIUS).
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -1- SIMILARITY: CONTAINS 2 XYNZ-TYPE CELLULOSE-BINDING DOMAINS (CBD).
CC
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DR	EMBL; D13325; BA02584.1; -
DR	HSSP; P09850; 1XNB.
DR	InterPro; IPR005084; CBM_6.
DR	InterPro; IPR001137; GH_11.
DR	Pfam; PF00457; Glyco_hydro_11; 1.
DR	Pfam; PF03422; CBM_6; 2.
DR	PRINTS; PR00911; GLYDRLASE11.
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW	Cellulose degradation; xylan degradation; hydrolase; glycosidase;
FT	SIGNAL; Repeat; 1.
FT	CHAIN 1 30 POTENTIAL.
FT	CHIN 31 512 ENDO-1,4-BETA-XYLANASE A.
FT	DOMAIN 236 365 CELLULOSE-BINDING (POTENTIAL).
FT	DOMAIN 416 504 CELLULOSE-BINDING (POTENTIAL).
FT	ACT_SITE 124 124 NICLOPHILE (BY SIMILARITY).
FT	ACT_SITE 215 215 PROTON DONOR (BY SIMILARITY).
FT	DOMAIN 236 244 PRO-RICH.
FT	DOMAIN 279 477 2 X 61 AA APPROXIMATE REPEATS.
FT	REPEAT 279 340 1.
FT	REPEAT 416 477 2.
SO	SEQUENCE 512 AA; 55843 MW; 1E133CBFAIC139305 CAC64;
Query Match	42.9%; Score 448.8; DB 1; Length 512;
Best Local Similarity	46.2%; Pred. No. 1.4e-12;
Matches 90; Conservative 24; Mismatches 59; Indels 22; Caps 5	
Oy	7 TGYNNCTFFSYNNDHGIGVTTYNNGCGQFVSVMNSGCFVGKRMOGCTKNK-----58-
Dd	39 TGHGGVDLELMD-YGNTIMELNDGGTFSCQWSNIGALFRKG-----RKNRSOKTYO 91
Oy	59 -----YINFGSYNPNGNSLYSVGMNRNPLEIYEIVENFGTYPNSTGATKLGEVTS-DG 112
Dd	92 ELGDIVVEYGCDYRNPGNSYLCVGTMTNPLRYEVIESMGSMRP-PGARPKGTITQMMA 150
Oy	113 SVYDIPTQRORNOPSTIIETAFIFYQYVSRHRSSGSYNTANHFNAMAQGLTLGTWDYO 172
Dd	151 GTEYEIETTRVNQPSIDGTATPQQYVSVTSKRTSGTISVTEHFKQERRMGMRGKYEV 210
Oy	173 IVAVEGFSSGSASI 187
Dd	211 ALTVEGYQSSGYANV 225
RESULT 21	
ID	XYNL_TRIPE STANDARD; PRT; 229 AA.
AC	P36218;
DT	01-JUN-1994 (Rel. 29, Created)
DT	01-JUN-1994 (Rel. 29, Last sequence update)
DT	15-JUN-2002 (Rel. 41, last annotation update)
DE	Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (xylanase 1)
GN	XYNL.
OC	Trichoderma reesei (Hypocrea jecorina).
OC	Eukaryota; Fungi; Ascomycota; Peziziomycotina; Sordariomycetes;
OC	Hypochoales; Hypocreaceae; Hypocrea.
OX	NCBI_TaxID=51453;
RN	[1]
RA	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC	STRAIN-QM9414 / Rut C-30.
RX	MEDLINE=93103679; PubMed=1369024;
RT	Toerrien A., Mach R.L., Messner R., Gonzalez R., Kalkkinen N.,
RT	Harki A., Kubicek C.P.;
RT	"The two major xylanses from Trichoderma reesei: characterization of
RL	both enzymes and genes";
RL	Biotechnology 10:1461-1465(1992).
RN	[2]
RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RP	MEDLINE=95127663; PubMed=7827044;
RA	Toerrien A., Rouvinen J.;

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RT "Structural comparison of two major endo-1,4-xylanases from
RT Trichoderma reesei."
RL Biochemistry 34:847-856(1995).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC -----
DR EMBL: X69574; CAA49294.1; -.
DR PIR: S39155; S39155.
DR PDB: 1XYN; 08-AUG-95.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11.1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11.2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal; 3D-structure.
FT SIGNAL 1 51
FT CHAIN 1 52
FT ACT_SITE 126 126
FT ACT_SITE 215 215
FT ACT_SITE 215 215
SQ SEQUENCE 229 AA; 24583 MW; F9E8BFE1607038DB CRC64;

Query Match 42.8%; Score 446.9; DB 1; Length 229;
Best Local Similarity 51.3%; Pred. No. 3.8e-13;
Matches 98; Conservative 22; Mismatches 50; Indels 21; Gaps 6;

QY 1 QTTQPGTGYNGYFYSYWMDHGCVTYTNGPGGQFVSVMNSGFMFGKMGQPGTKNKVI 60
DB 58 INQVTC-----GQVSYSPSNTG-FSVNMWNTQDFVVGVCWTTGS-SAPI 99
QY 61 NFSSSYTPN-GNSTLSVYSGSRNPLLEYIVENGNTNPSGTAKLCEVSDGSVDIYR 119
DB 100 NFGSFSFVNSGTGLLSVYGMSTNPLVEYIMEDNHN-PAQGTVK-GTVISDGATYTIWE 157
QY 120 TORNOSIIGTATFYQYWSVRRNRHSSGSVNTANHFNMAAQGLTGTDYQIVAVEGY 179
DB 158 NTRNESPISGTAIFNOYISVRNSPRTSGTYTVONHFNMAASGLGLHGMNTQVVAVEGW 217
QY 180 FSSGSASITVS 190
DB 218 GSGSASQSVS 228

RESULT 22
XNLI_ASPAW STANDARD: PRT: 211 AA.
AC P55328; 012534;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I)
DE (1,4-beta-D-xylan xylanohydrolase I).
GN XYNA OR EXLA.
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC STRAIN-ARCC 11358;
RX MEDLINE=9516119; PubMed=7859305;
RA Hessel J.G.M., van Rotterdam C.O., Verbakel J.M.A., Roza M., Maat J.,
RA van Gorcom R.F.M., van den Hondel C.A.M.J.J.;
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RT "Isolation and characterization of a 1,4-beta-endoxylanase gene of A.
RT awamori."
RL Curr. Genet. 26:228-232(1994).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X78115; CAA55005.1; -.
DR HSHP: P33557; 1BK1.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11.1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11.2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 27
FT CHAIN 1 27
FT ACT_SITE 106 106
FT ACT_SITE 197 197
FT ACT_SITE 197 197
SQ SEQUENCE 211 AA; 22627 MW; 86EFBE12A69022 CRC64;

Query Match 41.5%; Score 434; DB 1; Length 211;
Best Local Similarity 47.3%; Pred. No. 1.2e-12;
Matches 89; Conservative 26; Mismatches 63; Indels 10; Gaps 5;

QY 6 GTGYNNGYFYSYWMDHGCVTYTNGPGGQFVSVMNS-SCNFYGGKMGQPGTKNKVINS 63
DB 30 GINVQVY-----NGNIGDFTYDES-AGTFSMWEDSDDFVGLGIMTGGSSN-AITYS 82
QY 64 GSYNPN-NSYLSVYSGSRNPLLEYIVENGNTNPSGTAKLCEVSDGSVDIYR 122
DB 83 AEYSASGSSSLAYLAWGVNYPQAEYIVLEDYGDNPSSATSLGTYVSDSTVOVCTDTR 142
QY 123 VNQPSIIGTATFYQYWSVRRNRHSSGSVNTANHFNMAAQGLTGTDYQIVAVEGY 182
DB 143 TNESITGTSFTFYQYFVSRESTRSGTYTVANHFNMAQNGFQNSDINQYVMAVEMSGA 202
QY 183 GSASITVS 190
DB 203 GSASVTIS 210

RESULT 23
XNLI_ASPNG STANDARD: PRT: 211 AA.
AC P55329;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I)
DE (1,4-beta-D-xylan xylanohydrolase I).
GN XYNA.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=97045991; PubMed=8890913;
RA Krengel U., Dijkstra B.W.,
RA "Three-dimensional structure of Endo-1,4-beta-xylanase I from
RA Aspergillus niger: molecular basis for its low pH optimum."
RA J. Mol. Biol. 263:70-78(1996).;
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CC -1- FUNCTION: HAS A LOW PH OPTIMUM (3.0).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL: A19535; CA01470.1; -
DR PDB: 1UKR; 24-DEC-97.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PRO00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 1 28
FT ACT_SITE 106 211
FT ACT_SITE 106 106
FT ACT_SITE 197 197
FT DISULFID 119 138
SQ SEQUENCE 211 AA; 22641 MW; 82BBEBE12ED79303 CRC64;

Query Match 41.5%; Score 434; DB 1; Length 211;
Best Local Similarity 47.3%; Pred. No. 1.2e-12;
Matches 89; Conservative 27; Mismatches 62; Indels 10; Gaps 5;

QY 6 GTGYNNGYFYSYWNDGHGVTYTNPGGQFSYVMSN--SGNFVGGKGMPGTRKNVYNS 63
DB 30 GINYQVNT-----NGLDGFYTDSE-AGTFSMYMEDGVSDPVVGLGWTTS-SKATYIS 82
QY 64 GSYNPNNG-NSLYSVYSGMSNPLIEYIYVENFGTYPNSGATKLGKLVTSYDGYDIYRQR 122
DB 83 AEYSASGSSSYLAVYGMWNYVPOAEYIYVEDGYDYNPCSAATSLGTVYSDGSTRYQCTDTR 142
QY 123 VNOPSITGATFYQYVSVYRNHRSSGSVNTANHFMAAQQGLTGTMDYQIYAVGGRSS 182
DB 143 TNEPSITGSTRFTQYFSVRESTRISGTYVANHFMFAHFGNSDFNYQVAVBAMSGA 202
QY 183 GSASITVS 190
DB 203 GSASVTIS 210

RESULT 24
XYN1_ASPTU STANDARD: PRT: 211 AA.
AC P55331; 012568;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I)
DE (1,4-beta-D-xylan xylanohydrolase I).
GN XYN1 OR XLNA
OS Aspergillus tubingensis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillius.
OX NCBI_TaxID=5068;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NM756;
RA MEDLINE=94344036; PubMed=8065265;
RA de Graaf L.H., van den Broeck H.C., van Ooijen A.J.J., Visser J.;
RT "Regulation of the xylanase-encoding xlna gene of Aspergillus
RL tubingensis.";
Mol. Microbiol. 12:479-490(1994).
```

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RN [2]
RP REVISIONS.
RA de Graaf L.H., van den Broeck H.C., van Ooijen A.J.J., Visser J.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL: L26988; AAB05996.1; -
DR HSP: P55329; 1UKR.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PRO00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 27
FT CHAIN 1 28
FT ACT_SITE 106 211
FT ACT_SITE 106 106
FT ACT_SITE 197 197
SQ SEQUENCE 211 AA; 22576 MW; 1A88D06C57080D4 CRC64;

Query Match 41.3%; Score 432; DB 1; Length 211;
Best Local Similarity 47.3%; Pred. No. 1.5e-12;
Matches 89; Conservative 25; Mismatches 64; Indels 10; Gaps 5;

QY 6 GTGYNNGYFYSYWNDGHGVTYTNPGGQFSYVMSN--SGNFVGGKGMPGTRKNVYNS 63
DB 30 GINYQVNT-----NGLDGFYTDSE-AGTFSMYMEDGVSDPVVGLGWTSSN-ALITYS 82
QY 64 GSYNPNNG-NSLYSVYSGMSNPLIEYIYVENFGTYPNSGATKLGKLVTSYDGYDIYRQR 122
DB 83 AEYSASGSSSYLAVYGMWNYVPOAEYIYVEDGYDYNPCSAATSLGTVYSDGSTRYQCTDTR 142
QY 123 VNOPSITGATFYQYVSVYRNHRSSGSVNTANHFMAAQQGLTGTMDYQIYAVGGRSS 182
DB 143 TNEPSITGSTRFTQYFSVRESTRISGTYVANHFMFAHFGNSDFNYQVAVBAMSGA 202
QY 183 GSASITVS 190
DB 203 GSASVTIS 210

RESULT 25
XYN3_ASPAK STANDARD: PRT: 211 AA.
AC P33557;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 3 precursor (EC 3.2.1.8) (Xylanase 3)
DE (1,4-beta-D-xylan xylanohydrolase 3) (Xylanase C).
GN XYN3
OS Aspergillus awamori (var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillius.
OX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-34.
RC STRAIN=IFO 4308;
RA MEDLINE=93005082; PubMed=1368843;
RA Ito K., Iwashita K., Iwano K.;
RT "Cloning and sequencing of the xynC gene encoding acid xylanase of
```

RT Aspergillus kawachii.":
RL Biocsi. Biotechnol. Biochem. 56:1338-1340(1992).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 29-210.
RC STRAIN-IFO 4308;
RX MEDLINE=99127851; PubMed=9930661;
RA Fushinobu S., Ito K., Kono M., Wakagi T., Matsuzawa H.;
RT "Crystallographic and mutational analyses of an extremely acidophilic
and acid-stable xylanase: biased distribution of acidic residues and
importance of Asp-37 for catalysis at low pH."
RL Protein Eng. 11:1121-1128(1998).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
HYDROLASES).

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CC EMBL: S45138; AAC60542.1; .
CC EMBL: D14848; BAA03576.1; .
CC PIR: JCI198; JCI198.
CC PDB: 1BK1; 26-MAR-99.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_2; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 211 ENDO-1,4-BETA-XYLANASE 3.
FT ACT_SITE 106 106 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 197 197 PROTON DONOR.
FT DISULFID 119 138
SQ SEQUENCE 211 AA; 22560 MW; 68BFE90EBFEFFCC CRC64;

Query Match 41.2%; Score 430.9; DB 1; Length 211;
Best Local Similarity 44.0%; Pred. No. 1,6e-12;
Matches 88; Conservative 28; Mismatches 53; Indels 31; Gaps 6;

QY 21 GH-----GGVYTT--NG-----PGGQFSVMSN--SGNFYGGKQW 51
DB 12 GHAFAPVPQPYLVSRSAGINVQNYGNLADFTYDESAGFSSMYWEDGVSDFYVGLGW 71
QY 52 QPGTKNKYINFGSGYNPNNG-NSYLSYVGSRNPLEIYIVENFGTYNPGTAKIGEYTS 110
DB 72 TTGSSN-AISYSAEYSAGSSSYLAIVGVWVNPQAEIYIVEDYGVNPGSSATSLGTAYS 130
QY 111 DGSVVDIYRTQRPVNPSTIGATFYQYWSVRNHRSSSVNTANFNMAOQGLTGTM 170
DB 131 DGSYVQCTDRTNRPSTIGTISTFTQYFSVRSSTSTSGTVYANFNMAOAGFNSDEN 190
QY 171 YQIVAVEGYFSSGASITVS 190
DB 191 YQVMAVEAMSGASGASVITIS 210

RESULT 26
XNNA_RUMFL
ID XNNA_RUMFL STANDARD; PRT; 954 AA.
AC P29126;
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bifunctional endo-1,4-beta-xylanase Xyla precursor (EC 3.2.1.8).
GN XNNA.

OS Ruminococcus flavefaciens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae;
OC Ruminococcus.
OX NCBI_TaxId=1265;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=17;
RX MEDLINE=9226318; PubMed=1584021;
RA Zhang J.-X., Flint H.J.;
RT "A bifunctional xylanase encoded by the xyna gene of the rumen
cellulolytic bacterium Ruminococcus flavefaciens 17 comprises two
dissimilar domains linked by an asparagine/glutamine-rich sequence."
RL Mol. Microbiol. 6:1013-1023(1992).
CC -1- FUNCTION: XYLANASE DOMAIN 1 RELEASES MORE XYLO-OLIGOSACCHARIDES
AND DOMAIN 2 MORE XYLOSE.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY
G (FAMILY 11 OF GLYCOSYL HYDROLASES).
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY
F (FAMILY 10 OF GLYCOSYL HYDROLASES).

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CC EMBL: Z11127; CAA77476.1; .
CC PIR: S18043; S18043.
CC PIR: S20907; S20907.
CC HSSP: P48793; 1XND.
DR InterPro: IPR001137; GH_11.
DR InterPro: IPR001000; Glyco_hydro_10.
DR Pfam: PF00331; Glyco_hydro_10; 1.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00134; GLHYDRLASE10.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; 1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Multifunctional enzyme;
Repeat; Signal.
FT SIGNAL 1 27
FT CHAIN 28 954
FT DOMAIN 28 244 BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE Xyla.
FT DOMAIN 245 622 ASN/GLN/TRP-RICH (LINKER).
FT DOMAIN 623 954
FT ACT_SITE 122 122 XYLANASE DOMAIN 2.
FT ACT_SITE 223 223 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 774 774 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 884 884 NUCLEOPHILE (BY SIMILARITY).
SQ SEQUENCE 954 AA; 111362 MW; 1033567D4B526EBD CRC64;

Query Match 39.2%; Score 410; DB 1; Length 954;
Best Local Similarity 41.4%; Pred. No. 2.1e-10;
Matches 84; Conservative 33; Mismatches 66; Indels 20; Gaps 6;

QY 4 QPGTGNNGYFYSVNNDGSGVTTNGSGGQFSVMSNSGPNVG--GKGMPGRTKNK--- 58
DB 32 QOTRGNVGGYDEEMNNGQCOASNNPGASFTCSWSNIEFNLMRGNVYSOKKNYAF 91
QY 59 ---VINGSGSYNPNGNSYLSYVGSRNPLEIYIVENFGTYNP--STGATRLGEYTS 113
DB 92 GNIVLTVDVEYETPRGNSYMCYGVWTRNPLMEIYIVEGGDMRPENDEYK-GIYSANGN 150
QY 114 VYDIYRTQRPVNPSTIGATFYQYWSVRNHRSS-----GSVNTANFNMAOQGLT 165
DB 151 TYDIKRTKRYNPQSLDGTATFPQYWSVRSYSGSANNQNTNMYKGTIDYVTKHPDAWSAAGLD 210

Oy	166	LGTMDYOL-VAVEGFSSGASMI	187
		1: :	
Dd	211	MSGTLYEVSINIEGRNSGANV	233
RESULT 27			
ID	XYND_RUMFL	STANDARD:	PRT: 802 AA.
AC	053317:		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Xylanase/Beta-xylanase precursor [Includes: Endo-1,4-beta-xylanase		
DE	(EC 3.2.1.8) (Xylanase); Endo-beta-1,3-1,4 glucanase (EC 3.2.1.73)		
DE	(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase)].		
CN	XYND.		
OS	RumInnococcus flavofaciens.		
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae;		
OC	RumInnococcus.		
OX	NCBI_TaxID=1265;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=17.		
RX	MEDLINE=93259938; Pubmed=8491715.		
RA	Flinn H.J., Martin J., McPherson C.A., Daniel A.S., Zhang J.-X.;		
RT	"A bifunctional enzyme, with separate xylanase and beta(1,3-1,4)-		
RT	glucanase domains, encoded by the xynd gene of RumInnococcus		
RT	flavofaciens.";		
RL	J. Bacteriol. 175:2943-2951(1993).		
CC	-1- FUNCTION: CONTAINS TWO CATALYTIC DOMAINS WITH XYLANASE AND ENDO-		
CC	BETA-1,3-1,4 GLUCANASE ACTIVITIES.		
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic		
CC	linkages in xylans.		
CC	-1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages		
CC	in beta-D-glucans containing 1,3- and 1,4-bonds.		
CC	-1- PATHWAY: Xylan degradation.		
CC	-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY		
CC	G (FAMILY 11 OF GLYCOSYL HYDROLASES).		
CC	-1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 16 OF		
CC	GLYCOSYL HYDROLASES.		
CC	-----		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; S61204; AMB26620.1; .		
DR	HSSP; P23904; IAKK.		
DR	InterPro; IPR003305; CBM_Cenc.		
DR	InterPro; IPR001137; GH_11.		
DR	InterPro; IPR000757; Glyco_hydro_16.		
DR	Pfam; PF00457; Glyco_hydro_11.1.		
DR	Pfam; PF00722; Glyco_hydro_16.1.		
DR	Pfam; PF00218; CBM_4_9.1.		
DR	PRINTS; PRO0911; GLHYDLASE11.		
DR	PRINTS; PRO0737; GLHYDLASE16.		
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.		
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.		
DR	PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.		
KW	Xylan degradation; Hydrolase; Glycosylase; Signal;		
KW	Multifunctional enzyme.		
FT	SIGNAL	1	31
FT	CHAIN	32	802
FT	DOMAIN	32	244
FT	DOMAIN	245	523
FT	DOMAIN	524	555
FT	ACT_SITE	124	124
FT	ACT_SITE	226	226
FT	ACT_SITE	684	684
FT	ACT_SITE		
FT	POTENTIAL.		
FT	XYLANASE/BETA-GLUCANASE.		
FT	A (XYLANASE).		
FT	B.		
FT	LINER.		
FT	C (BETA-GLUCANASE).		
FT	NUCLEOPHILE (BY SIMILARITY).		
FT	PROTON DONOR (BY SIMILARITY).		
FT	NUCLEOPHILE (BY SIMILARITY).		

FT	DOMAIN	524	529	POLY-THR.
FT	DOMAIN	532	543	POLY-THR.
FT	DOMAIN	546	553	POLY-THR.
SO	SEQUENCE	802 AA:	890911 MM;	2880A689647284AF CRC64;
Query Match		37.6%;	Score 392.5;	DB 1; length 802;
Best Local Similarity		39.4%;	Pred. No. 9,1e-10;	
Matches	80; Conservative	31;	Mismatches	67; Indels 25; Gaps 6
OY	7	7	7	7
DB	37	37	37	37
OY	59	59	59	59
DB	97	97	97	97
OY	117	117	117	117
DB	157	157	157	157
OY	166	166	166	166
DB	214	214	214	214
RESULT 28				
XYNA_NEOPA STANDARD: PRT: 607 AA.				
ID	XYNA_NEOPA	P29127;		
AC	01-DEC-1992 (Rel. 24, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Bifunctional endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (XYLA).			
GN	XYNA.			
OS	Neocallimastix patriciarum (Rumen fungus).			
OC	Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;			
OC	Neocallimasticeae; Neocallimastix.			
OX	NCBI_TaxID=4758;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93023832; PubMed=1406248;			
RA	Gilbert H.J., Hazlewood G.P., Laurie J.I., Orpin C.G., Xue G.P.:			
RT	"Homologous catalytic domains in a rumen fungal xylanase: evidence for gene duplication and prokaryotic origin."			
RL	Mol. Microbiol. 6:2065-2072(1992).";			
CC	-1- FUNCTION: HYDROLYSES XYLAHS INTO XYLOBIOSIDE AND XYLOSE.			
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xylans.			
CC	-1- PATHWAY: xylan degradation.			
CC	-1- SIMILARITY: THE 43 AA REPEATS ARE SIMILAR TO THOSE IN PIROMYCES SP. XYNA, MANA, MANB AND MANC.			
CC	-1- SIMILARITY: THE N-TERMINAL AND C-TERMINAL PARTS BELONG TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).			
CC	-----			
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CC	-----			
DR	EMBL; X65526; CAA46498.1; -.			
DR	PIR; S21392; S21392.			
DR	HSSP; P33357; IBK1.			
DR	InterPro; IPR002883; CBD_5.			
DR	InterPro; IPR001137; GH_11.			
DR	Pfam; PF00457; Glyco_hydro_11; 2.			
DR	Pfam; PF02013; CBM_10; 2.			
DR	PRINTS; PR00911; GLHYDRASE11.			
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 2.			
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 2.			

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U01037; AAA21848.1; -.
DR HSSP; P36218; 1XN.
DR InterPro; IPR001137; GH_11.
DR Pfam; PF00457; Glyco_hydro.11; 2.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.
KW Cellulose degradation; xylan degradation; Hydrolase; Glycosidase;
KW Signal; Repeat
FT SIGNAL 1 25
FT CHAIN 26 608 ENDO-1,4-BETA-XYLANASE C.
FT DOMAIN 26 262 XYLANASE DOMAIN 1.
FT DOMAIN 263 285 SER-RICH (LINKER).
FT DOMAIN 286 529 XYLANASE DOMAIN 2.
FT DOMAIN 530 543 SER-RICH (LINKER).
FT ACCT_SITE 142 142 NUCLEOPHILE (BY SIMILARITY).
FT ACCT_SITE 237 237 PROTON DONOR (BY SIMILARITY).
FT ACCT_SITE 409 409 NUCLEOPHILE (BY SIMILARITY).
FT ACCT_SITE 501 501 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 608 AA; 66415 MW; 7EA338016F5857CE CMC64;

Query Match 28.6%; Score 299.3; DB 1; Length 608;
Best Local Similarity 33.0%; Pred. No. 6;4e-06;
Matches 69; Conservative 32; Mismatches 71; Indels 37; Gaps 7;

QY 8 GYNG-----YFYSWNODHGVTYNGRGCGQFYSVNMNSGNPVGCKGMQPTKN 57
Db 313 GGNSSVYTGNVGSSPHYETIYQG-GNNMFTFYNGYTKASWNGTDFLARVGRKYDEKH 371
QY 58 KVINFE-----SGSYNPNCNSYLSYVGWSRNPLEYIYEENFTYVPSTCAT 103
Db 372 TYEELGIDAYKMKSKGSGAGCVN-----YIGIGWIVDPLVEYIYIDDM--FN-KKGAN 423
QY 104 KL---GEVTSDSGVYDIYRTQRYVNQPSIGTATFYQYSVRRNRSSGYSNTANHFNAW 159
Db 424 LLGGRKEEFYVDGDTYETWMTFRQPSISIKGTQTFPQYFSYRKARSCHIDITAHMKW 483
QY 160 AAGGLTGTMDYQIVAVEGYFSSASIT 188
Db 484 EELGMKMKMYEAKYLVEAGGSGSPDVT 512

RESULT 30
XYNA_PIRSP STANDARD: PRT: 625 AA.
AC Q12667;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (1,4-beta-D-xylan
DE xylanohydrolase) (Xylanase A) (XLA).
GN XYNA.
OS Ptilomyces sp.
OC Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
OC Neocallimastacaceae; Ptilomyces.
OX NCBI_TaxID=45796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96094325; PubMed=7493964;
RA Fauriol G., Pomyl T., Black G.W., Hazlewood G.P., Gilbert H.J.;
RT "The conserved noncatalytic 40-residue sequence in cellulases and
RT hemicellulases from anaerobic fungi functions as a protein docking
RT domain."
RL J. Biol. Chem. 270: 29314-29322(1995).
CC -I- FUNCTION: HYDROLYZES 1,4-BETA LINKED POLYSACCHARIDE BACKBONES OF
CC XYLANS, ONE OF THE MAJOR HEMICELLULOSE COMPONENTS IN HARDWOODS AND
CC SOFTWOODS. IT IS MORE ACTIVE AGAINST XYLORRIOSE THAN
CC XYLOTETRAOSE, HAS TRACE ACTIVITY AGAINST XYLORRIOSE. THE MAJOR
CC PRODUCTS RELEASED FROM HYDROLYSTS OF XYLODIGOSACCHARIDES ARE
CC XYLORRIOSE AND XYLORRIOSE. THE RETREATED 40 AA DOMAIN IS INVOLVED

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CC IN BINDING THE CELLULASE-HEMICELLULOSE COMPLEX.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: xylan degradation.
 CC -1- DOMAIN: CONSISTS OF AN N- AND C-TERMINAL CATALYTIC DOMAINS LINKED
 CC TO A MIDDLE REITERATED DOMAIN. ONLY THE C-TERMINAL CATALYTIC
 CC DOMAIN IS ACTIVE.
 CC -1- SIMILARITY: THE 42 AA REPEATS ARE SIMILAR TO THOSE IN MANA, MANB
 CC AND MANC; AND TO THOSE OF N.PATRICIARUM XYNA.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X91858; CAA62969.1; -
 DR HSSP: F09850; 1XNB.
 DR InterPro: IPR002883; CBD_5.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 2.
 DR Pfam: PF02013; CBM_10; 2.
 DR PRINTS: PR00911; GLHYDRASE1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; FALSE.NEG.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; FALSE.NEG.
 DR KMW: xylan degradation; Hydrolase; Signal; Repeat.
 FT SIGNAL 1
 FT CHAIN 20 625
 FT DOMAIN 20 354
 FT DOMAIN 255 279
 FT DOMAIN 259 278
 FT REPEAT 259 268
 FT REPEAT 269 278
 FT DOMAIN 284 372
 FT REPEAT 284 325
 FT REPEAT 331 372
 FT DOMAIN 374 403
 FT DOMAIN 404 625
 FT ACT SITE 510
 FT ACT SITE 603
 FT SEQUENCE 635 AA; 68049 MW; 9DA959BA17290922 CRC64;
 Query Match 25.6%; Score 267.3; DB 1; Length 625;
 Best Local Similarity 26.2%; Pred. No. 0.00017;
 Matches 62; Conservative 41; Mismatches 67; Indels 67; Gaps 10;
 Oy 4 OPGTGYN-----GYFSYWD-GHGVTYNGP 31
 Db 388 QPTGQSNNSSTNTNFCSTKSHGQSYETSNKVGSIQGYELMADSGNNSATFYS-- 445
 Oy 32 GQFSVNMNSGTFVCGKMGQPGTKNKVYNFSG--SYNPN-----S 72
 Db 446 DGSFSCSRNAKDLCSG-----LSFDSTKTYTQOLGHMYADEFLVKONIQNDYS 496
 Oy 73 YLSVYGSRNPLEIYIYENF-GTYNPS--TGATKLEVTSDGSVYDIYRTQVNPSSII 129
 Db 497 YVGIGYTRNPLVEFYVDNMLSGMRPGDWGNKKKHDFITDGAKYTYEYENTRG-PSID 555
 Oy 130 GTATFYQWYVRNRHSSGSVNTANHNMAOGLTGTM-DYOIVAVEGYFSSGSA 185
 Db 556 GNTTFKQYFISROARDCGITDITAHFEQWEKLCMRGKMEAKVLCBAGSTSGSCTS 612

DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Muramidase-2 precursor (EC 3.2.1.17) (1,4-beta-N-
 DE acetylmuramoylhydrolase) (peptidoglycan hydrolase) (Pg-hydrolase-2)
 DE (Lysosyme).
 OS Enterococcus hirae.
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 NCBI_TaxID=1354;
 RP [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-73.
 RC STRAIN-ATCC 9790;
 RX MEDLINE-92165737; PubMed-1347040;
 RA Chu C.-P., Kariyama R., Daneo-Moore L., Shockman G.D.;
 RT "Cloning and sequence analysis of the muramidase-2 gene from
 RT Enterococcus hirae."
 RL J. Bacteriol. 174:1619-1625(1992).
 RN [2]
 RP FUNCTION.
 RC STRAIN-ATCC 9790;
 RX MEDLINE-89327152; PubMed-2753858;
 RA Dollinger D.L., Daneo-Moore L., Shockman G.D.;
 RT "The second peptidoglycan hydrolase of Streptococcus faecium ATCC 9790
 RT covalently binds penicillin."
 RL J. Bacteriol. 171:4355-4361(1989).
 RN [3]
 RP FUNCTION.
 RC STRAIN-ATCC 9790;
 RA Del Mar Lleo M., Canepari P., Satta G.;
 RT "Thermosensitive cell growth mutants of Enterococcus hirae that
 RT elongate at non-permissive temperature are stimulated to divide by
 RT parental autolytic enzymes."
 RL J. Gen. Microbiol. 139:3099-3117(1993).
 CC -1- FUNCTION: MAY WORK IN CONCERT WITH AND POTENTIATE THE PROCESSIVE
 CC HYDROLYTIC ACTION OF MURAMIDASE-1, WHICH REQUIRES BINDING OF THE
 CC ENZYME TO NONREDUCING ENDS OF GLYCAN CHAINS. HYDROLYSIS IN THE
 CC MIDST OF GLYCAN CHAINS WOULD INCREASE THE NUMBER OF BINDING SITES
 CC FOR MURAMIDASE-1. MAY FUNCTION IN FACILITATING SEPTUM FORMATION
 CC AND CELL SEPARATION. ACTIVE ON M.LIUREUS CELL WALLS AND ON E.HIRAE
 CC CELL WALL FRACTIONS. BUT NOT ACTIVE ON E.HIRAE INTACT CELL WALLS.
 CC CAN COVALENTLY BIND PENICILLIN.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-
 CC acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan
 CC heteropolymers of the prokaryotes cell walls.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOGLYCAN
 CC BINDING.
 CC -1- SIMILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES.
 CC -1- SIMILARITY: CONTAINS 6 LYSM REPEATS.
 CC -----
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 CC -----
 DR EMBL: M77639; AAA24776.1; -
 DR PIR: A42296; A42296.
 DR HSSP: P22629; 1SMD.
 DR InterPro: IPR002901; Amidase_4.
 DR InterPro: IPR002482; LYSM.
 DR Pfam: PF01476; LYSM; 6.
 DR Pfam: PF01832; Amidase_4; 1.
 DR SMART: SM00047; Lys2; 1.
 DR SMART: SM00257; Lysm; 6.
 DR SMART: SM00257; Lysm; 6.
 KM Hydrolase; Glycosidase; Bacteriolytic enzyme; Cell wall;
 KM Cell division; Septation; Repeat; Signal.
 FT SIGNAL 1
 FT CHAIN 50 666
 FT REPEAT 257 299
 FT REPEAT 338 380
 FT REPEAT 414 456
 FT MURAMIDASE-2.
 FT LYSM 1.
 FT LYSM 2.
 FT LYSM 3.


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FT REPEAT 489 531 LYSM 4.
FT REPEAT 565 607 LYSM 5.
FT REPEAT 623 665 LYSM 6.
SQ SEQUENCE 666 AA: 70670 MW: FFOX/FAFCDB10BA3 CRC64:

Query Match 15.7%; Score 163.6; DB 1; Length 666;
Best Local Similarity 17.5%; Pred. No. 6.4;
Matches 70; Conservative 28; Mismatches 68; Indels 234; Gaps 16;

OY 7 TGYNGCYFS-YW-----N 19
DB 161 TFSFGNGYYAGTWKSNKSYDTACTLGRYATDPGYAGKLNNTTGYLTYPDPASGN 220
OY 20 DGHGVTYNTPGP-GQFSYVMSNSGNFVGKGMQPT 55
DB 221 AG-GGTTTNGGNTGTNTSGTSGN-SGGSATTTCTTTVSGDSVNGISHTGTTMAQ 278
OY 56 -----KKKVI-----NFGSYNPGNS-----72
DB 279 LIEWNNIKNNFTYPCOKLTIKGQSGASSTTNTGNASSGNTSGTNTSGTGOATGAKY 338
OY 73 -----YLSVGMNRNPLEIYIVENFTY-----NPSTGAT 103
DB 339 TVKSGDSVWKIANDHGISMOLIEWNNIKNNFTYPCQOLVSKSGSSASGTSNTSGTNT 398
OY 104 -----KLGEVTSQSVYDIYRTQRYNQPSITIGATFYQWYVR-----142
DB 399 SGNNTANTGTTTS-GSYTYTVKAGESV-----WSVSNKFCISMOLIQNNNIK 443
OY 143 -----NHRSSGYNFANHN-----AMA--Q 161
DB 444 NNFTYPCOKLTIVKGGSSSNASTSTANNKNTASSNTSGATGATYTVKAGESWGVANK 503
OY 162 OGTLTGTM-----DYOIVAVEGEFFSSGASITV 189
DB 504 NGISMOLIEWNNIKNNFTYPCOKLTIVKGGSSKASATPATI 543

RESULT 32
ISOA_PSEAV
ID ISOA_PSEAV STANDARD: PRT: 776 AA.
AC P10342;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Isoamylase precursor (EC 3.2.1.68).
GN IAM.
OS Pseudomonas amyloclaterosa.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=32043;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=SB-15;
RX MEDLINE=88243808; PubMed=3379068;
RA Amenura A., Chakraborty R., Fujita M., Nouni T., Futai M.;
RT "Cloning and nucleotide sequence of the isoamylase gene from an
RT Pseudomonas amyloclaterosa SB-15.";
RL J. Biol. Chem. 263:9271-9275(1988).
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN=JD210;
RX MEDLINE=91064385; PubMed=2248978;
RA Chen J.H., Chen Z.Y., Chow T.Y., Chen J.C., Tan S.T., Hsu W.H.;
RT "Nucleotide sequence and expression of the isoamylase gene from an
RT isoamylase-hyperproducing mutant, Pseudomonas amyloclaterosa JD210.";
RL Biochim. Biophys. Acta 1087:309-315(1990).
RN 13
RP SEQUENCE OF 744-776 FROM N.A.
RC STRAIN=SB-15;
RX MEDLINE=89327147; PubMed=2753857;
RA Amenura A., Fujita M., Futai M.;
RT "Transcription of the isoamylase gene (iam) in Pseudomonas
RT amyloclaterosa SB-15.";

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RL J. Bacteriol. 171:4320-4325(1989).
[4]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RP MEDLINE=98387895; PubMed=9719642;
RX Katsuya Y., Mezaki Y., Kubota M., Matsuura Y.;
RA "Three-dimensional structure of Pseudomonas isoamylase at 2.2-A
RT resolution.";
RT J. Mol. Biol. 281:885-897(1998).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(1,6)-D-glucosidic branch
CC linkages in glycogen, amylopectin and their beta-limit dextrins.
CC -1- INDUCTION: BY MALTOSE.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY. ISOAMYLASE SUBFAMILY.
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CC
CC EMBL: J03871; AAA25854.1; -
CC DR EMBL: X13378; CAA31754.1; -
CC DR PIR: A28109; A28109.
CC DR PDB: 1BR2; 12-AUG-98.
CC DR InterPro: IPR000461; Alpha-amylase.
CC DR InterPro: IPR004193; Isoamylase-N.
CC DR Pfam: PF00128; alpha-amylase-N.
CC DR Pfam: PF02922; isoamylase-N; 1.
CC KW Hydrolase; Glycosidase; signal; 3D-structure.
CC FT SIGNAL 1 26
CC FT CHAIN 27 776
CC FT ACT_SITE 401 401
CC FT ACT_SITE 481 481
CC FT ACT_SITE 536 536
CC FT DISULFID 410 422
CC FT DISULFID 546 616
CC FT DISULFID 738 766
CC FT CONFLICT 8 8
CC FT CONFLICT 126 126
CC FT CONFLICT 169 171
CC FT CONFLICT 386 386
CC FT CONFLICT 413 416
CC FT CONFLICT 454 489
CC FT A -> G (IN REF. 1).
CC FT F -> C (IN REF. 1).
CC FT GAS -> AH (IN REF. 1).
CC FT L -> V (IN REF. 1).
CC FT GAYT -> AVH (IN REF. 1).
CC FT SGIDLFAEPMAIGNSYOLGGFPGGSENNGLFPROS ->
CC TWICLRNLGSPSATITSNVDSRRVRYVEMSVPRQ (IN
CC REF. 1).
CC FT WP -> S (IN REF. 1).
CC FT AFRKAHPA -> RSARHIP (IN REF. 1).
CC FT CONFLICT 650 657
CC FT CONFLICT 657 657
CC FT CONFLICT 657 657
SQ SEQUENCE 776 AA: 83626 MW: F738BF8040246169 CRC64;

Query Match 14.9%; Score 155.3; DB 1; Length 776;
Best Local Similarity 10.9%; Pred. No. 20;
Matches 74; Conservative 26; Mismatches 60; Indels 517; Gaps 18;

OY 13 YFYSYNNDDHG--GVTYNGPCQ-----FVWWSMS 42
DB 59 YLTS---AGYVOESATITLSPAGSGVNAVTVSVSSIKAGITGAVYGYGRAMGPWWPFA 115
OY 43 GNEVGGKGMQPG-----TRNKVI-----60
DB 116 SNW--GKSGQAGFVSDVDANGDRFNPNKLLLDPRYAQESQDPLNPSNONGNVFASGASYR 173
OY 61 -NFGSYNPG-----70
DB 174 TTDGGLYAPKGVVLPSTOSTGTPRAOKDDVIEVHVGRFTEQDTSPAOYRGTYGA 233
OY 71 ---NSYL-----74
DB 234 GLKASTLASIGTAVAEFLPVQETONDANDVVPNSDANQNTGNTENFSPDRRYANKA 293
OY 75 -----SVGNSRNPLEIYV- 88

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Db 294 AGGPTAEFQAMQAFHNAGIKYVMDVYVNTAEGTWTSSDPTTATYISMRGLDNATYFE 353
OY 89 -----IVENFGTYN----- 97
Db 354 LTSGNOYFYDNTGIGANFNFTYNTVAQNLIVDSLAVANTMGVDGFRFDLASVGLNSCLNG 413
OY 98 -----PSTGAT----- 103
Db 414 AYTAAPNCPCNGYNFDAADSNVAINRLREFYVPAAGSGGLDLFAEPAIGNSYQLG 473
OY 104 -----KLGEYTSQGSYVDIYRTORVNO----- 125
Db 474 GFPQGSSEWNGLEFRDSLROAQNELGSMT-----PSIIGTATFYQY----- 137
OY 126 -----PSIIGTATFYQY----- 137
Db 527 NSINFIDVHDMGLKDVYSCNGANNSQAMPYGPSDGTSTYNSWDOGMSAGTGAADVQR 586
OY 138 -----MSV----- 140
Db 587 AARTGMAFEMLSAGTPLMOGDEYLRTLQCNNAVNLDSANMLTYSMTTDOSNFYTFEQ 646
OY 141 -----RRNH-----RSSGSV-----NTANHFNMAAQGLTLGTM DY 171
Db 647 RLIAFRKAHPALRPSSWYSGSLTWYQPSGAVADSNVWNTSNVATAYAINGPSLSDSNS 706
OY 172 QIVAVEGYFSSGSASIT 188
Db 707 IYVAYNGW-----SSSVT 719

RESULT 33
ID ISOA_PSESP STANDARD: PRT: 776 AA.

AC P26501:
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Isoamylase precursor (EC 3.2.1.68).
GN IAM.
OS Pseudomonas sp. (strain SMP1).
OC Bacteria: Proteobacteria.
OX NCBI_TaxID:306;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 27-44.
RX MEDLINE=89381677; PubMed=2778432;
RA Tognoni A., Carrera P., Galli G., Lucchese G., Camerini B.,
Grandi G.,
RT Cloning and nucleotide sequence of the isoamylase gene from a strain
of Pseudomonas sp. [1]
RL J. Gen. Microbiol. 135:37-45(1989).
CC CATALYTIC ACTIVITY: Hydrolysis of alpha-(1,6)-D-glucosidic branch
linkages in glycogen, amylopectin and their beta-limits dextrans.
CC INDUCTION: BY MALTOSE.
CC SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY, ISOAMYLASE SUBFAMILY.
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CC EMBL: M25247; AAA25855.1; -
DR EMBL: A10909; CA000929.1; -
DR PIR: A37035; A37035.
DR HSSP: P10342; 1BF2.
DR InterPro: IPR000461; Alpha_Amylase.
DR InterPro: IPR004193; Isoamylase_N.
DR Pfam: PF00128; Alpha_Amylase_1.
DR Pfam: PF02922; Isoamylase_N; 1.

KW Hydrolyase; Glycosidase; signal.
FT SIGNAL 1 26
FT CHAIN 27 776 ISOAMYLASE
FT ACT_SITE 401 401 BY SIMILARITY.
FT ACT_SITE 481 481 BY SIMILARITY.
FT ACT_SITE 536 536 BY SIMILARITY.
FT ACT_SITE 410 422 BY SIMILARITY.
FT DISULFID 546 616 BY SIMILARITY.
FT DISULFID 738 766 BY SIMILARITY.
SO SEQUENCE 776 AA; 83656 MR; A5E4C02EF026A3A4 CRC64;

Query Match 14.9%; Score 155.3; DB 1; Length 776;
Best Local Similarity 10.9%; Pred. No. 20;
Matches 74; Conservative 26; Mismatches 60; Indels 517; Gaps 18;

OY 13 YFYSYNDHG---GYTYTNGPGQ-----FSVMSKNS 42
Db 59 YLYS--AGYVOESATYTLSPAGSGVAVATVPSSIKAGITGAVYGYRANGPMPYA 115
OY 43 GNFFVGKGMOPG-----TKNKVI----- 60
Db 116 SNM--GKSGAGSYSDVDANGDRPNPKLLDPRAEVSODPLNPSNONGVFAAGASYR 173
OY 61 -NFGSYNPG----- 70
Db 174 TTDGSIYAPKGVVLVSTOSTGTKPTRAKQDVIYEVHVGFTEDPTSIPOYRGTYGA 233
OY 71 ---NSYL----- 74
Db 234 GLKASYLASLGVTAVEFLPVQETONDANDVYVNSDANONWGYMTENYFSPDRRYAVNKA 293
OY 75 -----SVYGSRNPLIEY- 88
Db 294 AGGPTAEFQAMQAFHNAGIKYVMDVYVNTAEGTWTSSDPTTATYISMRGLDNATYFE 353
OY 89 -----IVENFGTYN----- 97
Db 354 LTSGNOYFYDNTGIGANFNFTYNTVAQNLIVDSLAVANTMGVDGFRFDLASVGLNSCLNG 413
OY 98 -----PSTGAT----- 103
Db 414 AYTAAPNCPCNGYNFDAADSNVAINRLREFYVPAAGSGGLDLFAEPAIGNSYQLG 473
OY 104 -----KLGEYTSQGSYVDIYRTORVNO----- 125
Db 474 GFPQGSSEWNGLEFRDSLROAQNELGSMT-----PSIIGTATFYQY----- 137
OY 126 -----PSIIGTATFYQY----- 137
Db 527 NSINFIDVHDMGLKDVYSCNGANNSQAMPYGPSDGTSTYNSWDOGMSAGTGAADVQR 586
OY 138 -----MSV----- 140
Db 587 AARTGMAFEMLSAGTPLMOGDEYLRTLQCNNAVNLDSANMLTYSMTTDOSNFYTFEQ 646
OY 141 -----RRNH-----RSSGSV-----NTANHFNMAAQGLTLGTM DY 171
Db 647 RLIAFRKAHPALRPSSWYSGSLTWYQPSGAVADSNVWNTSNVATAYAINGPSLSDSNS 706
OY 172 QIVAVEGYFSSGSASIT 188
Db 707 IYVAYNGW-----SSSVT 719

RESULT 34

ID AMYG_RHIOR STANDARD: PRT: 604 AA.

AC P07683;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Glucoamylase precursor (EC 3.2.1.3) (Glucon 1,4-alpha-D-glucosidase)

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OS Rhizopus oryzae (Rhizopus delemar).
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC Rhizopus.
ON NCBI_TaxID=64495;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SAM0034;
RA Ashkari T., Nakamura N., Tanaka Y., Kiuchi N., Shibano Y.,
RA Tanaka T., Amachi T., Yoshizumi H.;
RT "Rhizopus raw-starch-degrading glucoamylase: its cloning and
RT expression in yeast.";
RL Agric. Biol. Chem. 50:957-964(1986).
RN [2]
RP HOMOLOGY, AND PREDICTED SECONDARY STRUCTURE.
RA Tanaka Y., Ashkari T., Nakamura N., Kiuchi N., Shibano Y.,
RA Amachi T., Yoshizumi H.;
RT "Comparison of amino acid sequences of three glucoamylases and their
RT structure-function relationships.";
RL Agric. Biol. Chem. 50:965-969(1986).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
CC glucose residues successively from non-reducing ends of the chains
CC with release of beta-D-glucose.
CC -1- MISCELLANEOUS: RHIZOPUS GLUCOAMYLASE EXISTS IN MULTIPLE FORMS,
CC GLUC 1, GLUC 2, AND GLUC 3, ALL OF WHICH HYDROLYZE GELATINIZED
CC STARCH AT SIMILAR RATES, BUT ONLY THE LARGEST ONE (GLUC 1) IS ABLE
CC TO ADSORB RAW STARCH.
CC -1- SIMILARITY: BELONGS TO FAMILY 15 OF GLYCOSYL HYDROLASES.
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CC
CC EMBL: D00049; BAA00033.1;
CC PIR: JP0001; JP0001.
CC HSSP: P04064; 1GAI.
CC InterPro: IPR005036; CBM_21.
CC InterPro: IPR000165; GH_15.
CC Pfam: PF00723; Glyco_hydro_15; 1.
CC Pfam: PF00730; CBM_21; 1.
CC PRINTS: PR00736; GLHYDRLASE15.
CC PROSITE: PS00820; GLUCOAMYLASE. 1.
CC Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein;
KM Signal.
KW SIGNAL.
FT CHAIN 1 25
FT CHAIN 26 604
FT CHAIN 159 604
FT CHAIN 116 604
FT DOMAIN 26 109
FT DOMAIN 116 604
FT BINDING 279 279
FT ACT_SITE 336 336
FT ACT_SITE 339 339
FT ACT_SITE 340 340
FT ACT_SITE 604 AA: 65162 MW: 78421FIAMAA93ADB9 CRC64:
SO SEQUENCE
Query Match 14.7%; Score 153.3; DB 1; Length 604;
Best Local Similarity 15.8%; Pred. No. 15;
Matches 68; Conservative 25; Mismatches 71; Indels 267; Gaps 17;
QY 13 YF-----SYNNDGHC-----VTYNGGCGGGSVM 39
DB 18 YFSLVSAASIPSSASVQDSTYNQDSTFGKITYKNIAYSKRVTVYADG-----SDNW 72
QY 40 SNSGNFVGCGKWP--GTRKNKYINFGSYN----- 67
DB 73 NNNNGITIAASYSAPISGSNVEYWTFSASINGIKKEFIKYEYSGKTYTDNNNSANYVSTS 132
QY 68 -----PENGNSYLS----- 75

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DB 133 KPTTTTATATTTTAPSTSTTPPSRSEPAFTPTGNTSISSWIKOEGISRFAMLRNINPP 192
QY 76 -----YGWSRNLPI-----EY-----YIVENG 94
DB 193 GSATGFIASLSTAGPDYTYANTRDALTSNVIYIEYNTTSLGKNTILNVLKDYVTFSK 252
QY 95 TYNPSTGATKIGE--VTSDSVY-----DIYRTORVNOPSI 129
DB 253 TOSTSTVNCJGDEPKFNPNPASGYTGAMGRPQNDPAERATFTILFADSLTQTCKASVYT 312
QY 130 GT---ATF-----YQW-----SVRR 142
DB 313 GTLKPAIFKDLDDVYVWWSGCFDLMEEVNGVHFYTLWVRKGLLIGADFAKRNQDSTRA 372
QY 143 NRRSSGSVTANHF-----NAMO-----OGL-----TLGTMDOIVAV 176
DB 373 STYSSASTIANKISSFWWSNMWIOSVSYTGYSKGLDVSTLIANLGSVD----- 426
QY 177 EGYFSSGSASI 187
DB 427 DGFPTFGSEKI 437
RESULT 35
YD94.METUA
ID YD94.METUA STANDARD: PRT: 987 AA.
AC 058789;
DT 15-JUL-1998 (rel. 36, Created)
DT 15-JUL-1998 (rel. 36, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Hypothetical protein MJ1394.
GN MJ1394.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
ON NCBI_TaxID=2190;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weissflog K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uitterlbeck L.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- SIMILARITY: TO M. JANNASCHII MJ1393 AND A. FULGIDUS AF2028.
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CC
CC EMBL: U67579; AAB99404.1;
DB TIGR: MJ1394;
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 12 32 POTENTIAL.
FT TRANSMEM 958 978 POTENTIAL.
SO SEQUENCE 987 AA: 112360 MW: DJE628FFP28CA86D CRC64:
Query Match 14.4%; Score 151; DB 1; Length 987;
Best Local Similarity 12.2%; Pred. No. 47;
Matches 72; Conservative 22; Mismatches 78; Indels 420; Gaps 18;

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OY 139 -----SVRRNRSSGSVNTANHFN-AW----- 159
DB 446 KUKADLPRTGTPVDTTAPSPGNASTGV--TANSVTLAMNASTDUNVGTGVNYNGA 503
OY 160 -----AAGGLTIGCT-MDYQIVAVE--GYFSSGSASTVS 190
DB 504 NLATSVTGTATATISGLTAGTSTYTFIKAKDAAGNLAAASNAVTVS 548

RESULT 37
BCN5_CLOPE
ID BCN5_CLOPE STANDARD: PRT: 890 AA.
AC P08696:
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Bacteriocin BCN5.
GN BCN.
OS Clostridium perfringens.
OG Plasmid pip404.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OX Clostridium.
RN NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CPN50;
RX MEDLINE=88336297; PubMed=2901768;
RA Garnier T., Cole S.T.;
RT "Complete nucleotide sequence and genetic organization of the
bacteriocinogenic plasmid, pip404, from Clostridium perfringens.";
RL Plasmid 19:1134-1150(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CPN50;
RX MEDLINE=87057020; PubMed=2877971;
RA Garnier T., Cole S.T.;
RT "Characterization of a bacteriocinogenic plasmid from Clostridium
perfringens and molecular genetic analysis of the
bacteriocin-encoding gene.";
RL Bacteriol. 168:1189-1196(1986).
RN [3]
RP SEQUENCE OF 1-14 FROM N.A.
RC STRAIN-CPN50;
RX MEDLINE=89039249; PubMed=2460717;
RA Garnier T., Cole S.T.;
RT "Studies of UV-inducible promoters from Clostridium perfringens in
vivo and in vitro.";
RL Mol. Microbiol. 2:607-614(1988).
CC -1- FUNCTION: MAY FUNCTION AS AN IONOPHORE.
CC -1- INDUCTION: BY UV IRRADIATION.
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CC -----
CC
DR EMBL: M14481; AAA98248.1; -;
DR EMBL: M32882; AAA98249.1; -;
DR PIR: A30481; A30481.
DR InterPro: IPR003646; SH3_bac.
DR SMART: SM00287; SH3b_3.
KW Antibiotic; Bacteriocin; Plasmid.
FT DOMAIN 815 869 HTDROPHOBIC.
SQ SEQUENCE 890 AA: 96699 MW: 14558971C31C6C6 CRC64;

Query Match 13.8%; Score 143.7; DB 1; Length 890;
Best Local Similarity 14.4%; Pred No. 81;
Matches 61; Conservative 29; Mismatches 81; Indels 25; Gaps 15;
OY 1 OTIOGC-----TGYNNGYF-----YSYWN----- 19

DB 45 RTVSDGEITVLTISNEKNIVLVOYPTSSGYRQGVNTATSIIRKDDYSWNGSTPEPV 104
OY 20 -----DGHGVYITNPGGQFS---VNMSNGFNVGCKQM 52
DB 105 YDEPKTTTGILDPERRAVALYKVDGMTVAVDYTGKGLTFTSGLVHYEGSGSGTGG--- 160
OY 53 PGTKNKVINSGSYN-----PNCN----- 71
DB 161 -----GSFNGVAPGVEVPGCTFYENNAEYVGDGLYLRDANGNLIIPORSYVGDK 209
OY 72 -----SYLSYVGWSRNPLEYIYVEN---F 93
DB 210 ITVLDPGYTKOLALVOYPAGDVROGYVTNATNLTIRFNOYSWHNGSTSEEVLDENGHL 269
OY 94 GTYNPSTGATKLGVEITSSGSVYDIYRQR-----VNPSTIGTAT 133
DB 270 GSLNPEYEAATLLYE--KNGMKHVVYDTNKGPNPTKSGYVKEGAATRVDPDIPPSITNAOK 327
OY 134 FYQYWSVRNRHSSGSVNTANHFNA-----WAQGLTL----- 166
DB 328 I--VYGISGRGRELAAHYVGNCSNLSLVCAIHGEMDMADGIELTIRIGNLIEHPQNA 385
OY 167 GTMDYQIVAV-----EGY-----FSSGSAS 186
DB 386 GTNMNLSVITIPYANPDGLSEGTNNGPCRTIVGAVDCNRPDLGFSFGVPRYHSGSEP 445
OY 187 ITVS 190
DB 446 LSVS 449

RESULT 38
AMTB_PABPO
ID AMTB_PABPO STANDARD: PRT: 1196 AA.
AC P21543;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta/alpha-amylase precursor [Includes: Beta-amylase (EC 3.2.1.2);
Alpha-amylase (EC 3.2.1.1)].
OS Paenibacillus polymyxa (Bacillus polymyxa).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=1406;
RN [1]
RP SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-72;
RX MEDLINE=87165765; PubMed=2435707;
RA Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H.,
RT Tsukagoshi N., Uda S.;
RT "Cloning and nucleotide sequence of the gene coding for enzymatically
active fragments of the Bacillus polymyxa beta-amylase.";
RL Bacteriol. 169:1564-1570(1987).
RN [2]
RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-72;
RX MEDLINE=89123046; PubMed=2464578;
RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,
RT Tsukagoshi N., Uda S.;
RT "A single gene directs synthesis of a precursor protein with beta-
amylase and alpha-amylase activities in Bacillus polymyxa.";
RL J. Bacteriol. 171:375-382(1989).
RN [3]
RP SEQUENCE OF 1-776 FROM N.A.
RC STRAIN-ATCC 8523;
RX MEDLINE=87231094; PubMed=2438660;
RA Rhodes C., Strasser J., Friedberg F.;
RT "Sequence of an active fragment of B. polymyxa beta amylase.";
RL Nucleic Acids Res. 15:3934-3934(1987).
RN [4]
RP DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.
RX MEDLINE=91215008; PubMed=1827035;
RA Uozumi N., Matsuda T., Tsukagoshi N., Uda S.;

RT "Structural and functional roles of cysteine residues of Bacillus
RT polynymxa beta-amyLase."
RU Biochemistry 30:4594-4599(1991).
CC -1- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
CC PRODUCE MULTIFORM BETA-AMYLASES AND A 48 KDa ALPHA-AMYLASE AFTER
CC SECRETION.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
CC polysaccharides so as to remove successive maltose units from the
CC non-reducing ends of the chains.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION: BELONGS TO FAMILY 14 OF
CC GLYCOSYL HYDROLASES (BETA-AMYLASES).
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION: BELONGS TO FAMILY 13 OF
CC GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
CC EMBL: M15817; AA85446.1; -
CC EMBL: Y00150; CA68344.1; -
CC PIR: A29130; A29130.
CC PIR: A29108; A29108.
CC PIR: A32251; A32251.
CC HSSP: P36924; 1892.
CC InterPro: IPR000461; Alpha-amyLase.
CC InterPro: IPR005085; CBM_25.
CC InterPro: IPR001554; GH_14.
CC Pfam: PF00128; alpha-amyLase; 1.
CC Pfam: PF02806; alpha-hydro_14; 1.
CC Pfam: PF03423; alpha-amyLase_C; 1.
CC Pfam: PF03423; CBM_25; 2.
CC PRINTS: PR00750; BETAAMYLAZE.
CC DR PROSITE: PS00506; BETA-AMYLASE_1; 1.
CC DR PROSITE: PS00679; BETA-AMYLASE_2; 1.
CC DR MULTIFUNCTIONAL ENZYME: Hydrolyase, Glycosidase; Signal;
CC KW Polysaccharide degradation; Repeat.
CC -----
CC SIGNAL 1 35
CC FT CHAIN 36 1196 BETA/ALPHA-AMYLASE.
CC FT DOMAIN 36 454 BETA-AMYLASE.
CC FT REPEAT 455 558
CC FT REPEAT 565 668
CC FT DOMAIN 669 1196
CC FT DISULFID 118 126
CC FT ACT_SITE 124 124
CC FT ACT_SITE 198 198
CC FT ACT_SITE 118 118
CC FT MUTAGEN 126 126
CC FT MUTAGEN 358 358
CC FT MUTAGEN 1 1
CC FT CONFLICT 67 67 N->S (IN REF. 3).
CC FT CONFLICT 100 100 N->D (IN REF. 3).
CC FT CONFLICT 154 154 S->N (IN REF. 3).
CC FT CONFLICT 177 177 E->Q (IN REF. 3).
CC FT CONFLICT 227 228 NA->KS (IN REF. 3).
CC FT CONFLICT 330 330 G->S (IN REF. 3).
CC FT CONFLICT 425 425 N->S (IN REF. 3).
CC FT CONFLICT 493 493 D->A (IN REF. 3).
CC FT CONFLICT 532 532 S->L (IN REF. 3).
CC FT CONFLICT 559 559 A->T (IN REF. 3).
CC FT CONFLICT 665 665 A->T (IN REF. 3).
CC FT CONFLICT 681 681 D->N (IN REF. 3).
CC FT CONFLICT 725 728 T->A (IN REF. 3).
CC FT CONFLICT 736 736 APTS->VESP (IN REF. 3).
CC FT CONFLICT 741 741 N->K (IN REF. 3).
CC FT CONFLICT 741 741 N->S (IN REF. 3).
CC FT CONFLICT 758 758 S->N (IN REF. 3).
CC -----

SEQUENCE 1196 AA; 130893 MW; A41EA6B70F257064 CRC64;
Query Match 13.7%; Score 143.5; DB 1; Length 1196;
Best Local Similarity 10.1%; Pred. No. 1,4e+02;
Matches 75; Conservative 25; Mismatches 70; Indels 575; Gaps 20;
-----SYNDDG- 22
QY 2 TIQPGTGVNNGYFY-----
DB 462 TIYKKGFFSPYIHYRPAGSGWTAAPGVKMDAEISGYAKITVIDIGASQLEAFNDGN 521
QY 23 -----GGVYTNPGPGGFVSNWMSGNFVGC-KGWP-CTKNKI- 60
DB 522 NMDSNNTKNYSFSTGTSTYTPGNSG-----NAGTITGAPAGANPGGGGTNNVTVY 574
QY 61 -NFGG-SYNPNNSVLSVYG-----WS 80
DB 575 YKGFNSPYIHYRPAGSGWTAAPGVKMDAEISGYAKITVIDIGASQLEAFNDGN 634
QY 81 RNFLIEYIVENEGTYNP-----STGATKLEVT----- 109
DB 635 SNNTKNYLFSTGTSTYTPGNSGAGTIRTGAPSGVLSVYSTRYATDLNVEYGTPIOTEKL 694
QY 110 ----- 109
DB 695 SGVSLNVSTIYAPNSNGVEVTAQTEAPSGAFTSMDLGLSNPTSLNDSKOSIYFIMT 754
QY 110 -SDGS----- 113
DB 755 DRESNDGPDNDNGGNSNSNDOKRWKGGDFOCIINKLDYIKNMGTAIWITPYTMKSE 814
QY 114 -----VYDIYRT----- 120
DB 815 YAYHGYHTYDFAVDGLGTMKDLQELVKRKHDKNIYVWVYVNHNTGDFPGNGFAKAP 874
QY 121 ----- 120
DB 875 FDKADYHHNGDITDGDVNSNMQKLENGDVAGLDDLNENBPATANELKMWIKWLNENG 934
QY 121 -----ORVN-----OPTIGTAT----- 133
DB 935 IGLRLDYKHKVPKGLKLPDQANFTFMGEIFHGDPAYVGDYTRILDAALDPKMYTTIK 994
QY 134 ----- 133
DB 995 DVFHGDSMRKIKDRYSDDRYRDAQTNGVFTIDNHDKREFLDASGKPGANYDKMPQLKA 1054
QY 134 -----FYQVMS-----VRRNHR- 146
DB 1055 ALGFTLLTSRGIPITYGTGEGYSGDDPANRENNMNFANHDLXYITAKLVYVRRNHPALQ 1114
QY 147 SGS-----VNTANHFNAQAQGLTLGTMD----- 170
DB 1115 NSGQRKWKWDSEFYSGRKNCGDEALVFIN-----NSWNSQTRTIGNFNLNNGRFLTNO 1169
QY 171 -----YQIVAVEGYESSGSASITVS 190
DB 1170 LNSDSVOI-----NNGSITVTLA 1187

RESULT 39
FIND_ECOLI
ID FIND_ECOLI STANDARD; PRT; 878 AA.
AC P30130;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Outer membrane usher protein find precursor.
GN FIMD OR B4317.
OS Escherichia coli.
OC Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;
RN (1)

```

RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=90220509; PubMed=1970114;
RA Klemm P., Christiansen G.;
RT "The fimb gene required for cell surface localization of Escherichia
RL coli type 1 fimbriae."
RN Mol. Gen. Genet. 220:334-338(1990).
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Butland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RL region from 92.8 through 100 minutes."
RN Nucleic Acids Res. 23:2105-2119(1995).
CC -1- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF FIMBRIAL
CC SUBUNITS ACROSS THE OUTER MEMBRANE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
CC (by similarity).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
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CC
DR EMBL; U14003; CA35968.1;
DR EMBL; U14003; AAA97213.1;
DR EMBL; AE000502; AAC7273.1;
DR PIR; S11886; S11886
DR Ecocore; EGI0311; fimb.
DR InterPro: IPR000013; Fimb_usher.
DR Pfam: PF00577; Usher.1.
DR PROSITE; PS01151; FIMBRIAL_USHER.1.
KW Outer membrane; Transmembrane; Fimbria; Transport; Signal;
KW Complete proteome.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 878 OUTER MEMBRANE USHER PROTEIN FIMD.
FT DISULFID 855 877 POTENTIAL.
FT CONFLICT 143 148 ODATTAH -> RTLRT (IN REF. 1).
FT CONFLICT 352 402 DGSFOIFVPSVPLQRECHTYSITAGYRSGNQOEK
TREFOSTLLH -> VIARRELPYPIRFPPLNKAISLFI
YGRRIPIESRSKRPAPSRVYSN (IN REF. 1).
GGDNGSGSTGYAT -> EAMEIAEQATP (IN REF.
1).
FT CONFLICT 658 670
FT FT APGAKDAKVENQGTGRTDWR -> RLAKQMGKSKTRGAYR
LA (IN REF. 1).
FT CONFLICT 723 742
FT FT B2B86CC4FAB7B0F CRC64;
SO SEQUENCE 878 AA; 96482 MW; B2B86CC4FAB7B0F CRC64;

Query Match 13.6%; Score 142.2; DB 1; Length 878;
Best Local Similarity 16.2%; Pred. No. 92;
Matches 51; Conservative 20; Mismatches 46; Indels 198; Gaps 12;

OY 1 OTIOPGTY-----NNGEYSYWNDDHGVYTNNGP----- 32
DB 1 : ||| | ||| : ||| :
DB 71 QELPPGT-YRVDIYLNNGYMAT-----RDVTFTNGDSESGIVPCLTRPQALASGLNTAS 123
OY 33 -----GQSVNMSNSGNFVGKG-----WOPGTK 56
DB 124 VAGNNLADACVPLTTWQDATAHLVDGQORLNLITPQAFMSNRARQYIPPELMDPCIN 183
OY 57 NKVINEGSGYNPNNSLISYGVSRNPLIEYIYENFGTYNPSGATKLGVTSDGSVYD 116
DB 184 AGLLN-----YNFSGNS-----VON----- 198
OY 117 IYRTQVNOPSIITATFYQY-----WSVRNRHSSGSVYTNANFN 157
DB 199 -----RIGGSHYATLNLQSLGINTGAMRLRDNNTWVSNSDRSSGSKKKWQHIN 247

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OY 158 AMAOOG-----LTLTMDYQIVAVEGY----- 179
DB 248 TWLERDIILPLRSRLTLG-----DGYTGDLIFDGINFGAQLASDNNMLPDSORGFA 298
OY 180 -----FSSGSASTIV 189
DB 299 PVHIGIARGTAQVTI 313

RESULT 40
VG37_BPT2 STANDARD; PRT; 1341 AA.
ID VG37_BPT2
AC P07067;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Long tail fiber protein p37 (Protein gp37) (Receptor recognizing
DE protein).
GN 37.
OS Bacteriophage T2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OC NCBI_TaxID=10664;
OX [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=87112716; PubMed=3806672;
RA Riede I., Drexler K., Eschbach M.-L., Henning U.;
RT "DNA sequence of the tail fiber genes 37, encoding the receptor
RL J. Mol. Biol. 191:255-266(1986).
CC -1- FUNCTION: STRUCTURAL COMPONENT OF THE DISTAL-HALF TAIL FIBER.
CC -1- SUBUNIT: THE DISTAL HALF-FIBER CONTAINS TWO MOLECULES EACH OF GP36
CC AND GP37 AND ONE MOLECULE OF GP35.
CC -1- SIMILARITY: BELONGS TO THE TAIL FIBER FAMILY.
CC
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CC
DR EMBL; X04442; CAA28038.1;
DR PIR; S09579; S09579.
KW Fiber protein.
SO SEQUENCE 1341 AA; 143152 MW; 1B7981E7EA5FA7F5 CRC64;

Query Match 13.5%; Score 141.4; DB 1; Length 1341;
Best Local Similarity 11.2%; Pred. No. 2.2e+02;
Matches 80; Conservative 29; Mismatches 69; Indels 536; Gaps 24;

OY 1 OTIOPGTYNNGYTY-----STW-----ND 20
DB 222 QYVYPGCGEENGIMYLKRVRAKSGGTYHEIASAQTKNDEISWWTGTLTKLMGLND 281
OY 21 G----- 21
DB 282 GAMLRLNSLAIGTTADENTNNYCSPTPMGERTYALGDATGLKYIKQGYDLVGNNSV 341
OY 22 -----HGGVYTY-----NGPGQFVSNNNS 42
DB 342 ASITPDSFRSTRKALFGSSEGGG-TWTMPETNALLSVQOADVNNAGDQTHIIGVNSG 400
OY 43 G---NFGGKG----- 50
DB 401 GKMSHYFRGKQOTINIOKMEVNPGLKLVTDSENNVOFYANGTVSSIQRIKPDNGLVLT 460
OY 51 -----WOPGTK-----NK-----VINSGSYNPG----- 70
DB 461 GAPPDGIQLDAPTAADTKTILMAGGTRAGONKSYSTIKAGNSFNASGDRARETVREVG 520
OY 71 -----NSYLSAYVG- 78

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Db 521 DQGFHFYSQVAPAPGSTVGPDIOLRVNGCLLTAGSIYASGSITTESSILNVNGLSVNGO 580
OY 79 -----WS-----RNPLEIYIY-----90
Db 581 AKFGGTANALRTWMAEYGVIFRRSESNFTIPTNONEGESGDHSSLRPRVIGLNDGAVG 640
OY 91 -----ENF-----93
Db 641 LGRDSEIYDQNNALTTINSNRINANFRMQLGOSTYIDAECTDTVRPACAGSFVSQNNEN 700
OY 94 -----GTY-----NPSTGATK 104
Db 701 VRAPYMINRTDTSTVYPIIKORYVQNSCYSLGTLSTGDFRIHYHGGGNGSGTGPOK 760
OY 105 L-----GEVT-----SDGSV 114
Db 761 ADLAMOFRDGSFRSPNKEIEMAVITIGDGNITGCGNFANLNTLNKRTTYGVGMAGSSV 820
OY 115 YDIYTORVNOPSIIGTATFYQYWSVRRNRHSSGSV-----NPNAN 154
Db 821 VGMVFATVITPOSTGVTF-----KISGAGFNFKSYNQASIAEIVLRIGNNPK 870
OY 155 HENA--WAQGL-----TLGTMN--YQI-VAVEGYFS-----SGSASTY 189
Db 871 GINAVALMNRSDLSFNQIATMNTSDTYDVYFCEGYTALIVYSCSENSVTV 924

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RESULT 41

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SACB_STRSL STANDARD: PRT: 969 AA.
AC 055242:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Levensucrase precursor (EC 2.4.1.10) (Beta-D-fructofuranosyl
transferase) (Sucrose 6-fructosyl transferase).
GN PTP.
OS Streptococcus salivarius.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1304;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 25975; PubMed=8331080;
RX MEDLINE=9332232; PubMed=8331080;
RA Rathnam C., Giffard P.M., Jacques N.A.;
RT "The cell-bound fructosyltransferase of Streptococcus salivarius: the
cathoxyl terminus specifies attachment in a Streptococcus gordonii
model system.";
RL J. Bacteriol. 175:4520-4527(1993).
CC -I- CATALYTIC ACTIVITY: Sucrose + {(2,6)-beta-D-fructosyl}(N) =
glucose + {(2,6)-beta-D-fructosyl}(N+1).
CC -I- SUBCELLULAR LOCATION: SECRETED. CELL-WALL BOUND.
CC -I- SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.

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CC
CC EMBL: L08445; AAA71925.1;
DR InterPro: IPR003469; Glyco_hydro_68.
DR Pfam: PF02435; Glyco_hydro_68; 1.
DR TIGRfams: TIGR01168; YSIRK_signal; 1.
KW Transferrase; Glycosyltransferase; Signal; Cell wall.
FT SIGNAL 1
FT CHAIN 1
FT SEQUENCE 969 AA: 103983 MW: D389B5B32AC735A CRC64:

```

Query Match 13.5%; Score 140.6; DB 1; Length 969;
 Best Local Similarity 17.2%; Pred. No. 1.3e+02;
 Matches 73; Conservative 19; Mismatches 78; Indels 254; Gaps 19;

```

OY 6 GTG-----YNN-----GYF-----14
Db 230 GTGTSILYRNLMKDIVASFLKQDSKLAVPEFKADITIIIMPATVDAQTAKKEIDVWDSW 289
OY 15 -----YSYNN-----GHGYTYTNKPGCGFSVN-- 38
Db 290 PVQDAKSGVYSNMNGYQLYISAGAPNKNSHIILYLRKYGDNDFTHKMAGPIFGYNAL 349
OY 39 -----WSNS-----GNFYGK--GMQ-----PGTKKV 59
Db 350 EDDQMGSGATVNSDGSGLYLYTKNDTSGCKLMQGLASATLNLAVENDEVYKSEVDNH 409
OY 60 INFSG-----SY-----NP-----NGNSYL-----74
Db 410 ILFGDNYHYQSYPRKFMSTFDDHNDGNPDRTDNYCLRDPHIIEDNGSRYLIFESNIGD 469
OY 75 -----SYGWSRNPLEIY-----IVENGY-----NPSTGATKGEV 108
Db 470 ENYQGEKQIYKSN-----YGGDAFNLSKFLNIVNNKHLNLSAMANGSIGILKLDON 523
OY 109 TSDGSVYDIYR-----TORVNOPSIIGTATFYQYWSVRRNRHRS-----146
Db 524 EKNPSVAELTYPLVTSNHWTDVEKPSYKMGCKYLLFTASINIKNSTAGCTVAAREAVG 583
OY 147 -----SGSVNANHNANAQGLTIGTDYQIVAVEGYFSSGS 184
Db 584 DDVVMGLGFVSDLSRGKRYPLNGSGVLTASVPADM-----RTSYSYAVPVEG--SSDT 636
OY 185 ASIT 188
Db 637 LLVT 640

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RESULT 42

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OM3A_RHILV
ID OM3A_RHILV STANDARD: PRT: 366 AA.
AC 005811:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Outer membrane protein Iiia precursor (OMP1iia).
GN ROPA.
OS Rhizobium leguminosarum (biovar viciae).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=387;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-31.
RC STRAIN-248;
RX MEDLINE=92104965; PubMed=1370281;
RA de Maagd R.A., Mulders I.H.M., Canter Cremers H.C.J.,
RA Lugtenberg B.J.J.;
RT "Cloning, nucleotide sequencing, and expression in Escherichia coli
of a Rhizobium leguminosarum gene encoding a symbiotically repressed
outer membrane protein.";
RL J. Bacteriol. 174:214-221(1992).
CC -I- FUNCTION: MAY ACT AS AN OUTER MEMBRANE PORE.
CC -I- SUBUNIT: FORMS CALCIUM-STABILIZED OLIGOMERS.
CC -I- SUBCELLULAR LOCATION: Outer membrane.
CC -I- DEVELOPMENTAL STAGE: REPRESSED IN THE BACTEROID FORM DURING
SYMBIOSIS.

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CC -I- PTM: ATTACHED COVALENTLY TO PEPTIDOLYCAN.
CC
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CC EMBL: M69214: AAA20488.1: ALT_SEQ.
CC PIR: S27656; S27656.
DR PIR: A43303; A43303.
DR Interfero: IPR003684; Porin_alpha.
DR Pfam: PF02530; Porin_2; 1.
KW Outer membrane; Signal; Antigen.
FT SIGNAL 1 22
FT CHAIN 23 366 OUTER MEMBRANE PROTEIN IITA.
SQ SEQUENCE 366 AA: 38969 MW: 66C4A4E5C0C91381 CRC64;

Query Match 13.4%; Score 140.1; DB 1; Length 366;
Best Local Similarity 17.4%; Pred. No. 23;
Matches 54; Conservative 17; Mismatches 36; Indels 203; Gaps 15;

QY 8 GYNNCGFYSYVNDGHC-----YTYNPGGCGFSVMSNSGNF----- 45
DB 130 GFRAGLFYSWMDGLGETDDIGSVTLHNSIRYQ-----ESGTFYAGLSVDELDGY 184
QY 46 -----VGCK-----GWC----- 52
DB 185 QGTFPTGVIPTGTTDFADGPNVGVAFGIGTAGAFSYQVYGMDVNDGAIKRMGTV 244
QY 53 ---PGTKRVINFGSSYPNPNNSYLSVYGSNRPLIEY-----YIVEN 92
DB 245 EIGPGT-----FGLAGYSSGPNSSYSSAEWA--VAEYAIKATDKLTPGRWHGVHPED 298
QY 93 FGTYNPSTGATKLGVEYTSQGSYVDIYRTQVNOPSLIGATFYQVYSVRNRHSSGSVNT 152
DB 299 F-----DG-----LGDA-----WKV----- 308
QY 153 ANHFNAQOGLTIGTMDYQV-----AVEGYSS----- 182
DB 309 -----GL---TVDYQIVENFYAKASVOYLDPDQDEDSISGFACSVSNHLVDAP 355
QY 183 ---GSASIT 188
DB 356 GLRIGSTTIS 365

RESULT 43
BIGA_SALTY STANDARD; PRT; 1953 AA.
ID BIGA_SALTY
AC P25927: P25928; Q9XCQ3;
DT 01-MAY-1992 (Rel. 22, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Putative surface-exposed virulence protein biga precursor.
GN BIGA OR STM3478.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN 11
RN SEQUENCE FROM N.A.
RC STRAIN-ATCC 14028;
RA Stojiljkovic I., Valentine P., Heffron F.,
RT Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN-LT2 / SGC1412 / ATCC 700720;
RX MEDLINE=21534948; Pubmed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
RA *Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.
RL Nature 413:852-856(2001).
RN [3]

RP SEQUENCE OF 1-765 FROM N.A.
RC STRAIN-LT2;
RX MEDLINE=91100301; Pubmed=1987123;
RA Wu J.Y., Siegel L.M., Kredich N.M.;
RT "High-level expression of Escherichia coli NADPH-sulfite reductase:
RT requirement for a cloned *cysG* plasmid to overcome limiting *trp*heme
RT cofactor.";
RL J. Bacteriol. 173:325-333(1991).
CC -1- CAUTION: Ref.3 sequence differs from that shown due to frameshifts
CC in positions 414 and 732.
CC
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CC EMBL: AF133696; AAD39458.1; -
CC DR EMBL: AE008859; AAL22340.1; -
CC DR EMBL: M64606; AAA27042.1; ALT_FRAME.
CC DR EMBL: M64606; AAA27043.1; ALT_FRAME.
CC PIR: C39200; C39200.
CC DR PIR: D39200; D39200.
CC StyGene: SG10437; biga.
CC Virulence; Repeat; Signal; Complete proteome.
FT SIGNAL 1 27
FT CHAIN 28 1953
FT
FT DOMAIN 101 252
FT REPEAT 101 103
FT REPEAT 104 113
FT REPEAT 114 122
FT REPEAT 123 133
FT REPEAT 134 144
FT REPEAT 145 155
FT REPEAT 156 166
FT REPEAT 167 177
FT REPEAT 178 188
FT REPEAT 189 199
FT REPEAT 200 210
FT REPEAT 211 221
FT REPEAT 222 232
FT REPEAT 233 243
FT REPEAT 244 252
FT CONFLICT 207 207
FT CONFLICT 514 514
FT CONFLICT 1698 1698
FT CONFLICT 1795 1798
FT CONFLICT 1836 1837
SQ SEQUENCE 1953 AA: 200150 MW: 611B3F1C954D91AE CRC64;

Query Match 13.4%; Score 139.8; DB 1; Length 1953;
Best Local Similarity 16.9%; Pred. No. 5.1e+02;
Matches 62; Conservative 30; Mismatches 62; Indels 212; Gaps 17;

QY 7 TGYNCG-----YFY-----SYNNDG----- 21
DB 1240 TTYNNDFTGSIAGTSYQOEIVNTGDMVAEDKSLVSGSFYFNEDEATLTLSGSAVEG 1299
QY 22 -----HGGVTVNPGCGGFSVMSNSGNFVG----- 47
DB 1300 GEMTITNLRANDSLQVNSGTTTATNGYSAITTVNGSDPKIMWTATGVIINGINPDAP 1359
QY 48 ---GKGWPGTKRVINFGSSYPNPNNSYLSVYGSNRPLIEYIVE--NFGYVNPST- 100
DB 1360 LNLGRGYNEGNO-----GTINVGDNAAVAISGTS-----YVINLVNSGTINWGRE 1407
QY 101 -----GATKLGVTSDG--SYV----- 115
DB 1408 QGKEDGTGCTGLIGIKNGCNATTINN-TADGVINAVADSDYAFGCKTAIINNGEINLLC 1466

OY 116 ----DIYRORVNOPIITGATFYQWVRNRH-----SSGSVNT----- 152
DB 1467 DSGCIVY-----ABGTGTCT-----QNDHNGTADIVIPDATTAPEGSIPTPPADP 1511
OY 153 -----ANHF-----NANAQGLTGTMDYOYVAVEGYRSS--- 182
DB 1512 NAAPOOLSNRYVGTNADSSGSLKANNLVIGDNVYDFTSGTADTTVVDNAFGSNIQ 1571
OY 183 GSASIT 188
DB 1572 GADNIT 1577
RESULT 44
WAPA_BACSU
ID WAPA_BACSU STANDARD: PRT: 2334 AA.
AC 007833:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 13-JUN-2002 (Rel. 41, Last annotation update)
DE Wall-associated protein precursor.
GN WAPA OR N17G.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RX MEDLINE=93302506; Pubmed=8316082;
RA Foster S.J.;
RT "Molecular analysis of three major wall-associated proteins of
RT Bacillus subtilis 168: evidence for processing of the product of a
RT gene encoding a 258 kDa precursor two-domain ligand-binding
RT protein."
RL Mol. Microbiol. 8:299-310(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-168 / BGSC1A1;
RX MEDLINE=95219088; Pubmed=7704263;
RA Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
RT "Cloning and sequencing of a 29 kb region of the Bacillus subtilis
RT genome containing the hut and wapa loci."
RL Microbiology 141:337-343(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-168 / BGSC1A1;
RX MEDLINE=97124196; Pubmed=8969509;
RA Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,
RA Miwa Y., Fujita Y.;
RT "Sequencing of a 65 kb region of the Bacillus subtilis genome
RT containing the hic and cel loci, and creation of a 177 kb contig
RT covering the gut-sacxy region."
RL Microbiology 142:3113-3123(1996).
CC -1- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,
CC MOTILITY, SECRETION OR DIFFERENTIATION
CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED
CC INTO THE MEDIUM.
CC -1- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE
CC 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE
CC C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED
CC MOTIF REPEATED 31 TIMES.
CC -1- SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME
CC SIMILARITY TO THE REPEAT IN E.COLI RBS GROUP OF PROTEINS (RBSA-D).
CC -----
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CC -----
DB EMBL: L05634; AAA22883.1; -

DR EMBL: D31856; BAA06656.1; -
DR EMBL: D29985; BAA06260.1; -
DR EMBL: D83026; BAA11683.1; -
DR EMBL: 299124; CAB15959.1; -
DR PIR: S32920; S32920.
DR Subtilisin; BGI0797; WAPA.
DR Interpro: IPR003305; CBM_Cenc.
DR Pfam: PF02018; CBM_4_9; 1.
DR Cell wall; Repeat; Signal; Complete proteome.
DR OR 32 (POTENTIAL)
FT CHAIN 1 28
FT SIGNAL 1 28
FT DOMAIN 1 2139
FT REPEAT 1021 2139
FT REPEAT 1021 1040
FT REPEAT 1042 1061
FT REPEAT 1063 1082
FT REPEAT 1083 1102
FT REPEAT 1109 1128
FT REPEAT 1129 1148
FT REPEAT 1150 1169
FT REPEAT 1174 1193
FT REPEAT 1199 1218
FT REPEAT 1219 1238
FT REPEAT 1246 1265
FT REPEAT 1267 1286
FT REPEAT 1290 1309
FT REPEAT 1312 1331
FT REPEAT 1352 1371
FT REPEAT 1372 1391
FT REPEAT 1419 1438
FT REPEAT 1440 1459
FT REPEAT 1461 1480
FT REPEAT 1487 1506
FT REPEAT 1508 1527
FT REPEAT 1529 1548
FT REPEAT 1569 1588
FT REPEAT 1583 1602
FT REPEAT 1608 1627
FT REPEAT 1628 1647
FT REPEAT 1651 1670
FT REPEAT 1671 1690
FT REPEAT 1692 1711
FT REPEAT 1712 1731
FT REPEAT 1732 1751
FT REPEAT 1753 1772
FT REPEAT 1775 1794
FT REPEAT 1820 1839
FT REPEAT 1840 1859
FT REPEAT 1861 1880
FT REPEAT 1887 1906
FT REPEAT 1908 1927
FT REPEAT 1929 1948
FT REPEAT 1969 1988
FT REPEAT 1983 2002
FT REPEAT 2008 2027
FT REPEAT 2028 2047
FT REPEAT 2051 2070
FT REPEAT 2071 2090
FT REPEAT 2093 2112
FT REPEAT 2120 2139
FT REPEAT 2134 2153
FT SEQUENCE 2334 AA; 258329 MW; B75138CCD278BAA3 CRC64;
SO
Query Match 13.4%; Score 139.7; DB 1; Length 2334;
Best Local Similarity 8.8%; Pred. No. 7.1e+02;
Matches 84; Conservative 32; Mismatches 61; Indels 773; Gaps 25;
OY 8 GYNN-----GYFYSYW----- 18
DB 629 GYNNATGYFDLSMKAVSATGYKVQVFNKGPEFLDNGTSMWTKGKIPTSIEIK 688
OY 19 -----NGCHG----- 23
DB 689 AGKVALHKGSGELDPINCPYTKNAGGOGAKRNYSFKIIAYNKDEALASPAPALP 748
OY 24 -----GVTYN----- 29
DB 749 DIAPKRVTVGLVTNTSSQTYVNLWEKVQNAKGYKNVINYNGKEYQSFVDGADAHWT 808
OY 30 -----GGQGFVN-----MSN-SGNEVG----- 47
DB 809 QNKNIWPTSEIKASYKLTLDGKGLALDPSVYNNANNGVKKKKYSFTLVAVDANG 868
OY 48 ----- 47
DB 869 ETIPTAFNPFTHEGAFLCTEEYWSIIDIPSGOLGATGNTVINEEDLSIDGRGQLG 928

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OY 48 -----GKGM-----QP----- 53
DB 929 SRTYNSLDSSDHLFGGQWADAFSTVISTDGMATIDEDATTHRTTKADGTQPTPGY 988
OY 54 ----- 53
DB 989 LELLETADOFILTKDQTNAYFNKKGKGLQKVVDGHNNAVTYVYNDKNOLTAITDASGRK 1048
OY 54 -----GTRKNVINF-----GSYN----- 67
DB 1049 LFTTDENGHVTSTPTKNNKVTYENDLLKKVTDGTGTVSYDSEGRVLYKQYSANS 1108
OY 68 -----PNCNSYLSYVGMGRNPL 84
DB 1109 TEAKPVFTEYSGHRLKAIKAKETVYVYADKKTLMLTPNCRKQOYGYNEAGNP 1168
OY 85 -----IEYV-----IYENFGT--- 95
DB 1169 OVIDAEGKLITNTFKYEGNNVEDVPNDVGTGKATESYQYDKGNVTSVKDAYGTETRY 1228
OY 96 -YRPSGTATKL-----GEVT-----SDGSYYDIY----- 118
DB 1229 ETKKNDVTKMDTEGNTVDIAYDGLDAVSETDQSGKSSAAVYDKYGMQIOSSKDLAS 1288
OY 119 ----- 118
DB 1289 TNLKGSFEAQSGMNLASKDRRKISVADKSGVLSGSKALEVLSQSTSACTDHGYS 1348
OY 119 RTQRY----- 123
DB 1349 ATOFVELPNTTYTTLGKIKITDLAKSRAVENIDLRDQKRIQIHNEYSALAGKNDWTK 1408
OY 124 -----NQPSLIGATFY-----Q 136
DB 1409 RQITFTFPANAGAAVYMEVDKDKDKGKAMFEVQLEKEVSSNPYONSSFTSATE 1468
OY 137 YMSVRNRHSSGSVNTANFN-----AWAQOQ-----LTIG 167
DB 1469 NMNV-----SGASVDEEGFNDVSLKAARTSASQGSVTKQTVVLGQSANCKPYVLTLL 1523
OY 168 TW-----DYQIYAVEGY-----FSSGS-----ASTIV 189
DB 1524 GMSKASSVKTDEKDYSLQANVTYADGSTGYNAKFEPSGTQEWNRRAVY 1573

RESULT 45
GUN_BACS6
ID GUN_BACS6 STANDARD: PRT: 941 AA.
AC P19424;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Endoglucanase precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
OS (Alkaline cellulase).
DE Bacillus sp. (strain KSM-635).
OC Bacteria: Firmicutes: Bacillales: Bacillaceae: Bacillus.
OX NCBI_TaxID=1415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91037937; PubMed=2230718;
RA Ozaki K., Shikata S., Kawai S., Ito S., Okamoto K.;
RT "Molecular cloning and nucleotide sequence of a gene for alkaline
RT cellulase from Bacillus sp. KSM-635."
RL J. Gen. Microbiol. 136:1327-1334(1990).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
CC linkages in cellulose.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
CC HYDROLASES).
CC -1- SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
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DR EMBL: M27420; AAA22304.1; -
DR PIR: S29043; S29043.
DR HSSP: 085465; 3A3H.
DR InterPro: IPR005086; CBM_17_28.
DR InterPro: IPR001347; GH_5.
DR InterPro: IPR001119; SLH.
DR Pfam: PF00150; cellulase. 1.
DR Pfam: PF00395; SLH; 3.
DR Pfam: PF03424; CBM_17_28; 2.
DR PROSITE: PS00659; GLYCOSYL_HYDROL_F5; 1.
DR PROSITE: PS01072; SLH_DOMAIN; 2.
KW Cellulose degradation; Hydrolase; Glycosylase; Signal; Repeat.
FT SIGNAL 1 29
FT CHAIN 30 941
FT DOMAIN 30 99
FT DOMAIN 40 99
FT DOMAIN 100 151
FT DOMAIN 152 225
FT ACT_SITE 373 373
FT ACT_SITE 485 485
FT ACT_SITE 485 485
SQ SEQUENCE 941 AA; 104628 MW; BEA2AC3B169BFADA CRC64;

Query Match 13.3%; Score 139.4; DB 1; Length 941;
Best Local Similarity 13.6%; Pred. No. 1,4e+02;
Matches 70; Conservative 26; Mismatches 61; Indels 356; Gaps 21;

OY 4 OPCTGYNNG----- 12
DB 373 EFSPPNNGGRLTNDKCKEAVKEAEPYIEMLRKGDMMILVGNPNMSQRPDLASDNP 432
OY 13 -----YFYSYNDGCG-----GVYTN 29
DB 433 DAENIMYVHEFTGSHGASHIGPECTPSERSNVANRYALDNGVAVFATPMGTISQAN 492
OY 30 GRGGR-----SVNMSNGNFVGKQKQPGTKNV----- 59
DB 493 GDGPRFDEADVWLFNLRKHNISWAN-----WSLTKKEISGAFPFELGRTDAVD 543
OY 60 -----INSGSY-----NP 68
DB 544 LDPGANQVAPBELSLSGEYVRARIKIEYTPIDRKTKLWDFMDGTGQFOVNGDSP 603
OY 69 N-----GNSY-----LSYVGSRN-----PLIEYIVE 91
DB 604 NKESTILSNNDALQIEGLVNSNDISEGNVMDVNRSLADGWSSEVDILGATELTIDVIVE 663
OY 92 N-----FGTNPSTGATKGLD-----VTSQGSYIDYRTOR 122
DB 664 EPTTVSIAIIPQAPAGMANP-TRAIKYEDDEFESPDGYKALVLTYSDDS----- 713
OY 123 VNQPSI-----IGTAF- 134
DB 714 ---PSLETTATSPEDNTMSNILLFVGTEDADVISLDTNIVSGTEIEIYIHDEKGTATLP 770
OY 135 -----YOYWSVRNRHSSG-----SVNTANFNA-----WA----- 160
DB 771 STFEDGTQGMW----HTSSGVKTAITIEANSMNLSMEYAVPEVKPSDGMATAPRLDF 827
OY 161 -QOGLTLGTMQIYAVEGYF-----SSGSAST 187
DB 828 WKDELVRGTSVY----ISFDYIDAVRASGAIS 858

RESULT 46
VG37_BPK3
ID VG37_BPK3 STANDARD: PRT: 1243 AA.
AC Q38394;
DT 15-DEC-1998 (Rel. 37, Created)
```

DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Long tail fiber protein p37 (Protein Gp37) (Receptor recognizing protein).
 GN 37.
 OS Bacteriophage K3.
 OC Viruses: dsDNA viruses, no RNA stage: Caudovirales: Myoviridae;
 OC unclassified Myoviridae.
 OX NCBI_TaxID=10674;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87112716; PubMed=3806672;
 RA Ride I., Drexler K., Eschbach M.-L., Henning U.;
 RT "DNA sequence of the tail fiber genes 37, encoding the receptor
 RT recognizing part of the fiber, of bacteriophages T2 and K3."
 RL J. Mol. Biol. 191:255-266(1986).
 CC 1- FUNCTION: STRUCTURAL COMPONENT OF THE DISTAL HALF TAIL FIBER. IT
 CC CONSTITUTES THE PART OF THE LONG TAIL FIBERS THAT RECOGNIZES THE
 CC BACTERIAL RECEPTOR.
 CC 1- SUBUNIT: THE DISTAL HALF-FIBER CONTAINS TWO MOLECULES EACH OF GP36
 CC AND GP37 AND ONE MOLECULE OF GP35.
 CC 1- MISCELLANEOUS: THE TWO GP37 PROTEIN CHAINS RUN IN PARALLEL. THE
 CC LENGTH OF THE DISTAL HALF-FIBER, WITH THE AMINO END NEAR THE
 CC CENTER KINK OF THE FIBER AND THE CARBOXYL END AT THE DISTAL TIP.
 CC THE OTHER POLYPEPTIDES ARE DISTRIBUTED UNIFORMLY ALONG THE LENGTH
 CC OF THE DISTAL HALF-FIBER.
 CC 1- SIMILARITY: BELONGS TO THE TAIL FIBER FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: X04747; CAA28445.1; -
 DR Fiber protein.
 KW SEQUENCE 1243 AA; 132990 MW; 115E6B9D0C695928 CRC64;
 SO
 Query Match 13.3%, Score 139.3; DB 1; Length 1243;
 Best Local Similarity 9.5%; Pred. No. 2.3e+02;
 Matches 79; Conservative 25; Mismatches 61; Indels 667; Gaps 22;
 QY 3 IOPG-----TCYNGYFYS----- 16
 DB 408 INPGLILKLVGSSNVQYADGNISIQPVKLDNELFLNSSNNTAGLFGAPSKVDGTRAI 467
 QY 17 YWNG-----H----- 22
 DB 468 QMNGGTREGONKNYIIKANGSNFENATGDRSRETFQVSDSGYFYAHRKAPTDEITG 527
 QY 23 -----GGVYTING-----PGGQ----- 34
 DB 528 RIEQFAGELNAKSNVENVKVGSLTVGGVTMSKGLNTGSSITIGOVKIGCTYDAL 587
 QY 35 -----FSV----- 37
 DB 588 RIMNSRYCAIFRSETSLHIPTNENEGENGAINNLRPFSTIELGTGTVMCLHDVHLNSG 647
 QY 38 -----NM----- 39
 DB 648 SSTGLLOVNSLTKTKICPVTINERNAALTLDSPSSSSANYLOGSKAGTKSMVVGIGA 707
 QY 40 -----SNSGNF----- 45
 DB 708 GNDLSLTSQSYGHGLVSDNFNVSISKPLKGNQOLGDTGNTGSGSGFANLNTLANKVN 767
 QY 46 -----VGKGNQPGT----- 55
 DB 768 SGFTYCATSGMYKFAIVTMQSTSTAFKIVGSGSGNSGLFTQCNIATIEIVLRTGNRPA 827
 QY 56 -----KKKVINFGSGSYNPNGNSY-LSVYGNRNPDLIEYIVENEGTY--- 96

DB 828 DLNAVLYTRTIGAFKNIAVN-----NVSQGTXYIYYVA-----GTVCNQ 867
 QY 97 ----- 96
 DB 868 LACEMACTENATISVIGINSSTQSPVDDLPDTAVAGOVANVNLVDSGKGRYEAESSEI 927
 QY 97 --NPSTG-----ATKIGEYV-----SPGSYVDIYRTQVNOPTSLGTATFYQVSVRR-- 142
 DB 928 AINSQTGIRIRSNADKTKGSAVTMLRNDGGSFYILFTKNDTD---GAATVNGENNSKRP 984
 QY 143 -----NHRSSGSVN----- 151
 DB 985 AINLTGGEVMMNNGIAVRSALFYNSINVDKSGNINFDKSGANRMRIFHAGDASGRN 1044
 QY 152 -----TANHF-----NANAQGLTIGTYDYQ 172
 DB 1045 IEIADETNYIAFEKABGAGANRFVYNATVSGVNMNSFGVNTSNALGNSITFGPDYTG 1104
 QY 173 I-----VAEGYF----- 180
 DB 1105 IKONGDGLDIYANNAQVFRQNGDLXSYKNINAPNYISDITLKSINFRIENALDKVE 1164
 QY 181 -----SSGSASITVS 190
 DB 1165 KLVGVYDKAEYIGGEAIEFEAGIVAOITLQVLPBAVRETEDSKGNKILTVS 1216
 RESULT 47
 FHUE.ECOLI
 ID FHUE.ECOLI STANDARD; PRT; 729 AA.
 AC P16869; P77292;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FhuE receptor precursor (outer-membrane receptor for Fe(III)-coprogen,
 DE Fe(III)-ferritoxamine B and Fe(III)-rhodotulic acid).
 GN FHUE OR B1102.
 OS Escherichia coli.
 OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=90286919; PubMed=2162465;
 RA Sauer U., Hantke K., Braun V.;
 RT "Sequence of the fhuE outer-membrane receptor gene of Escherichia
 RT coli K12 and properties of mutants."
 RL Mol. Microbiol. 4:427-437(1990).
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474(1997).
 RN 131
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitegawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiiuchi T.;
 RT "A 7.18-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map."
 RL DNA Res. 3:137-155(1996).

[4]
RN SEQUENCE OF 37-50.
RP STRAIN-K12;
RX MEDLINE-87194585; PubMed-3032906;
RA Sauer M., Hantke K., Braun V.;
RT "Ferric-coprogen receptor FhuE of Escherichia coli: processing and
sequence common to all TonB-dependent outer membrane receptor
proteins";
RL J. Bacteriol. 169:2044-2049(1987).
CC -1- FUNCTION: REQUIRED FOR THE UPTAKE OF IRON(III) VIA COPROGEN,
CC FERRIOXAMINE B, AND RHODOTOLUIC ACID.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -1- INDUCTION: FOR INDUCTION THE TONB AND THE EXBB PROTEIN HAVE TO
CC BE ACTIVE.
CC -1- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.

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CC or send an email to license@isb-sib.ch).

DR EMBL: X17615; CA35616.1; -;
DR EMBL: AE000210; AAC74186.1; -;
DR EMBL: D90745; BAA35909.1; -;
DR EMBL: D90746; BAA35917.1; -;
DR PIR: S09262; S09262.
DR PIR: A26875; A26875.
DR Ecocyc: EG10306; fhuE.
DR InterPro: IPR000531; TonB_box.
DR Pfam: PF00593; TonB_box.
DR PROSITE: PS00430; TONB-DEPENDENT_REC_1; 1.
DR PROSITE: PS01156; TONB-DEPENDENT_REC_2; 1.
DR Outer membrane; Iron transport; Transport; TonB box; Signal; Receptor;
KW Complete proteome.
FT SIGNAL 1 36
FT CHAIN 37 729 FHU RECEPTOR.
FT SITE 42 49 TONB BOX.
FT SITE 712 729 TONB C-TERMINAL BOX.
FT MUTAGEN 44 44 V->P: ABOLISHES TRANSPORT ACTIVITY.
FT MUTAGEN 46 46 V->P: ABOLISHES TRANSPORT ACTIVITY.
FT MUTAGEN 163 163 G->A,V,N,D,H: IMPAIRED TRANSPORT AND
FT GROWTH.
FT CONFLICT 363 363 G->C (IN REF. 1).
FT SEQUENCE 729 AA; 81232 MW; 68ACE7D110F76CD CRC64;
SO
Query Match 13.3%; Score 139; DB 1; Length 729;
Best Local Similarity 14.1%; Pred. No. 90;
Matches 73; Conservative 20; Mismatches 70; Indels 353; Gaps 19;
OY 8 GYNN-----GYFY-----YWN-DG- 21
DB 227 GYNNDSWLDRYNSEKTFEFGIVDADGLDTLTLASGYEQRIDVNSPTWGLPRMNTDGS 286
OY 22 -----IGV-----TYT 28
DB 287 SNSYDRASAPDMAYNDKEINKVFMTLKQGFADTQWATLNTATSEVEFSDKMYVDAYV 346
OY 29 NGPGGQFVNMSNSG---NFVGKGKMGPGTNNKV-----INFGSSY 66
DB 347 NKADGMLVGPYSNCGPFDYVGCTGWSNG-KRKVDALLDFADGSEYELFGROHNLMEFGSSY 405
OY 67 NPGNSYLSVYG-----MSRNPDI----- 86
DB 406 SKONRRYFSWANIFPDEIGSFYNFNGNFPQTDMSPOSADDDTTHMKSLYAATFVTLAD 465
OY 87 -----YYIENGTYNPSI----- 100
DB 466 PLHLILGARITNWRVDLTLYSMENKHTTPYAGLVFLIDNMWSTYASYSIFOPONDRDSS 525
OY 101 ----- 100

DB 526 GKYLAPITGNYYELGKSDMWSRLTTLAFRIEDQNVASTGTPIGNSGTAYKAVD 585
OY 101 -----GATK-----LGE 107
DB 586 GTFSGKVEEFLNGAITDNMQLTFATRYIAEDNMGNAVNPRLPTTYKMTFSRLPVME 645
OY 108 VTSQGSV-----YDIYRTORVNOPS--IIIGTATFYQWGVRRNRHSSGSVNTANH 155
DB 646 LTVGGGVWQNRVYTDTPYTGTFRAEDGSIALVDLFTIRY---VTKNFSLQGNV--NL 700
OY 156 FNMAAOGELTGTMDYQIVAVEG---YFSSGSASIT 188
DB 701 FDK-----TYD---TWNEGSIYVGTPEPNSFIT 724

RESULT 48
GUXB_CELFI
AC GUXB_CELFI STANDARD; PRT; 1090 AA.
ID P50899;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Exoglucanase B precursor (EC 3.2.1.91) (Exocellulohydrolase B)
DE (1,4-beta-cellulohydrolase B) (CBP120).
GN CBH OR CENE.
OS Cellulomonas fimi.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Micrococccineae; Cellulomonadaceae; Cellulomonas.
OX NCBI_TaxID=1708;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 456-461.
RC STRAIN-ATCC 484;
RX MEDLINE-96003898; PubMed-7575482;
RA Shen H., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;
RT "Cellulohydrolase B, a second exo-cellulohydrolase from the
RT cellulolytic bacterium Cellulomonas fimi.";
RL Biochem. J. 311:67-74(1995).
RN [2]
RP SEQUENCE OF 54-75.
RX MEDLINE-93209933; PubMed-8458833;
RA Meinke A., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;
RT "Cellulose-binding polypeptides from Cellulomonas fimi: endoglucanase
RT D (Cend), a family A beta-1,4-glucanase.";
RL J. Bacteriol. 175:1910-1918(1993).
RN [3]
RP SEQUENCE OF 54-78.
RX MEDLINE-94197708; PubMed-8147863;
RA Shen H., Tomme P., Meinke A., Gilkes N.R., Kilburn D.G.,
RA Warren R.A.J., Miller R.C. Jr.;
RT "Stereochemical course of hydrolysis catalysed by Cellulomonas fimi
RT Cend, a member of a new family of beta-1,4-glucanases.";
RL Biochem. Biophys. Res. Commun. 199:1223-1228(1994).
CC -1- FUNCTION: HYDROLYSE CELLOHEXAPOSE TO A MIXTURE OF CELLOTETRAOSE,
CC CELLOTRIOSE AND CELLOBIOSE, WITH ONLY A TRACE OF GLUCOSE. IT
CC HYDROLYSE CELLOPENTAPOSE TO CELLOTRIOSE AND CELLOBIOSE, AND
CC CELLOTETRAOSE TO CELLOBIOSE, BUT IT DID NOT HYDROLYSE CELLOTRIOSE.
CC HAS ALSO WEAK ENDOGLUCANASE ACTIVITY. HYDROLYSES GLUCOSIDIC BONDS
CC WITH INVERSION OF ANOMERIC CONFIGURATION.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
CC in cellulose and cellobiose, releasing cellobiose from the non-
CC reducing ends of the chains.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
CC (CBD).
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY L (FAMILY 48 OF GLYCOSYL
CC HYDROLASES).

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DR EMBL: L38827: AAB00822.1: -
 CC HSSP: P07986: 1EXG
 DR InterPro: IPR001919: Bac_cellose-bind.
 DR InterPro: IPR003961: FN_III.
 DR InterPro: IPR003962: FNIII_repeat.
 DR InterPro: IPR000556: Glyco_hydro_48.
 DR Pfam: PF00041: fn3: 3.
 DR Pfam: PF00553: CBM_2: 1.
 DR Pfam: PF02011: Glyco_hydro_48: 1.
 DR PRINTS: PR00014: FNTYPEIII.
 DR PRINTS: PR00844: GLYHYDRLASE48.
 DR ProDom: PD011903: Glyco_hydro_48: 1.
 DR SMART: SM00060: FN3: 3.
 DR PROSITE: PS00561: CBD_BACTERIAL: 1.
 KM Cellulose degradation; Hydrolase; Glycosidase; Repeat; Signal.
 FT SIGNAL 1 33
 FT PROPEP 34 53
 FT CHAIN 54 1090
 FT DOMAIN 54 699 EXOGLUCANASE B.
 FT DOMAIN 700 785 CATALYTIC (BY SIMILARITY).
 FT DOMAIN 794 884 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 891 978 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 989 1090 FIBRONECTIN TYPE-III 3.
 FT ACT_SITE 513 513 CELLULOSE-BINDING (BY SIMILARITY).
 FT DISULFID 990 1089 NUCLEOPHILE (BY SIMILARITY).
 FT DISULFID 990 1089 BY SIMILARITY.
 SO SEQUENCE 1090 AA: 114829 MW: 0468BD956F399 CMC64;

Query Match 13.3%; Score 138.7; DB 1; Length 1090;
 Best Local Similarity 11.5%; Pred. No. 1.9e+02;
 Matches 69; Conservative 34; Mismatches 76; Indels 423; Gaps 19;

OY 8 GYNGY-----FYSYMDGNGCYT----- 26
 |||
 DB 383 GYONPLAALALSTDPKLTSPKAPAKADMAASMOROLEFTYTLQASNGLAGATNSWDGA 442
 |||
 OY 27 -----YTNRP----- 31
 |||
 DB 443 YAOPTPTFYGMGTETAPVYDPPSNRFQMANGVORVALYLYASGNAOKKLLDKW 502
 |||
 OY 32 -----GGSFVS-----NMSN-----SGN----- 44
 |||
 DB 503 VPMVAVANISTDGAAMKVPSELKWTGKPDWTMAAAPGNGLVEVTSYGODVGVADTAR 562
 |||
 OY 45 ---FVGKGMQPTKKR----- 67
 |||
 DB 563 ALLEFYAAKSGDTASRDKAKALDAIWMANODPLGSAVETRGDKRPDDTYVANGDGIYI 622
 |||
 OY 68 PN-----GNSLYSV-----GMSR----- 81
 |||
 DB 623 PSCWMTGMPNGDVIKRGVSEFLDIRSFYKKDPNMSKYQTLFDGAEQFRHRTWAQTAVA 682
 |||
 OY 82 NPLIEYIYENCTYVPS-----GA 102
 |||
 DB 683 GALADYARLFDDGTTPTTAPTPTVPTGLAGVVTSTEATISMTASTDTRVTGYDYRGA 742
 |||
 OY 103 TKLG-----E 107
 |||
 DB 743 TKVGTATTTSTFDTGLTASTAVAYTVRAADAGNVSAPSALTVTTKAPPSDTTASVPA 802
 |||
 OY 108 VTSDGSV-----YDIYR-TQVNPQSI-----IGTATFYQY 137
 |||
 DB 803 ITSSSTANSVTTIGNSASTDNAGSGSLAGDYVRGATRAQTALTFTDTGLTASTAYEX 862
 |||
 OY 138 ----- 137
 |||
 DB 863 TVRADVAGNSAPSTAVSVTTKSDTTPDTTASVPAGLAAMVTETSAALTWNASTDNG 922
 |||
 OY 138 -----WSYRRNRSSGSVNTANHFANMAQGLTGT-KDYQVAVNE--GYFSSGSAST 188
 |||
 DB 923 GSGLKGYDYVRGATRVGSTTTA-----SYDTGTLTATTAAYQYTVRATDNAGNVSASAAALS 978
 |||

OY 189 VS 190
 ||
 DB 979 VT 980

RESULT 49
 FAND_ECOLI
 ID FAND_ECOLI STANDARD; PRT; 783 AA.
 AC P12050;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Outer membrane usher protein fand precursor.
 GN FAND.
 OS Escherichia coli.
 OC Plasmid pFK99.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TaxID=562;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B41;
 RX MEDLINE=89160266; PubMed=2564179;
 RA Roosendaal B., Bakker D., de Graaf F.K.;
 RT "The nucleotide sequence of the fand gene encoding the large outer
 membrane protein involved in the biosynthesis of K99 fimbriae.";
 RL Nucleic Acids Res. 17:1263-1263(1989).
 RN [2]
 RP SEQUENCE OF 1-20 FROM N.A.
 RA Roosendaal B., Gastra W., de Graaf F.K.;
 RT "The nucleotide sequence of the gene encoding the K99 subunit of
 enterotoxigenic Escherichia coli.";
 RL FEMS Microbiol. Lett. 22:253-256(1984).
 RN [3]
 RP SEQUENCE OF 770-783 FROM N.A.
 RC STRAIN-B41;
 RX MEDLINE=91312125; PubMed=1713284;
 RA Bakker D., Vader C.E.M., Roosendaal B., Mool F.R., Oudega B.,
 de Graaf F.K.;
 RT "Structure and function of periplasmic chaparrone-like proteins
 involved in the biosynthesis of K88 and K99 fimbriae in
 enterotoxigenic Escherichia coli.";
 RL Mol. Microbiol. 5:875-886(1991).
 CC -1- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF K99 FIMBRIAL
 SUBUNITS ACROSS THE OUTER MEMBRANE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
 (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
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DR EMBL: X13560: CAA1911.1: -
 DR EMBL: M35282: -; NOT_ANNOTATED_CDS.
 DR EMBL: X56001: CAA39473.1: -
 DR PIR: S02755; S02755.
 DR InterPro: IPR000015: Fimb_usher.
 DR Pfam: PF00577: usher: 1.
 DR PROSITE: PS01151: FIMBRIAL_USHER: 1.
 KM Outer membrane; Transmembrane; Fimbria; Transport; Signal; Plasmid.
 FT SIGNAL 1 23
 FT CHAIN 24 783 OUTER MEMBRANE USHER PROTEIN FAND.
 FT DISULFID 763 782 POTENTIAL.
 SO SEQUENCE 783 AA: 87156 MW: 23BDE3923A9B7069 CRC64;

Query Match 13.3%; Score 138.5; DB 1; Length 783;
 Best Local Similarity 14.9%; Pred. No. 1.1e+02;

Matches 71; Conservative 23; Mismatches 69; Indels 315; Gaps 20;

QY 9 YNNGYFYSYWMDGHC-----GWTYTN----- 29

DB 192 YGRGYKE-----HDKFTTDDVTLSPRAISLEGDLLIGDTYNTSLMDNISFYVOLRSN 246

QY 30 -----GP----- 31

DB 247 NAMTPRRRDYPIISIGIAKSNARVTVKONGVYLHSELYSPGPFHINNRGIRSGELVMT 306

QY 32 ---GGQ-----FSVWMSNGNF-----VGK--GWQPG----- 54

DB 307 VTEEDSEQOTRIPYVFIANLLSPGNYNYPFGICNKEATWEPDNIPAGSFDYGLNLT 366

QY 55 -----TKNV-----INFGSYNPG 70

DB 367 NASLLEPHYNSNAGICAVSIGSLGAVSYSGNISRAKNOLETDQGYSTANYSKNGANG 426

QY 71 -----NSLYSGMSRNP 84

DB 427 NLQIGKFSSEGYTOYANFDYRAPRKDKKEREYVTLTQCFPASNVLSTVGMKK----- 483

QY 85 IEY-----IVENFGTYNDS-TGATKLGSEVTSQSYDIYRTQRVNQPSTIGT 131

DB 484 --FYMDNSVYGANVSYTQNFQTVNASVNGSYSRG---DGAKSDYMLGFNINIPFRHND 537

QY 132 AFYQYWSYVRNHRSSG-----SYNTA----- 153

DB 538 RQFYNSGYTYN-RNSGIGFNGAFSEDYTKNENYVNAASAADNESVSLSTNTSSMFT 596

QY 154 -----NHFNMAQ-OGLTGTMD-----VOIVAVEG-FSSGSAS 186

DB 597 SASVSKNRSTNASTAAGIGALIGVKDGYVLTSMSSNSVAIYQMEGLAGAFITNGVES 654

RESULT 50

PM19.CHLPN STANDARD: PRT: 947 AA.

ID PM19.CHLPN Q92813; Q9JSE2;

AC 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Probable outer membrane protein pmp19 precursor (Polymorphic membrane protein 19).

GN PMP19 OR CPN0539 OR CP0213.

OS Chlamydia pneumoniae (Chlamydia pneumoniae).

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

NCBI_TaxID=83538;

OX NCBI_TaxID=83538;

RN 11

RC SEQUENCE FROM N.A.

RP STRAIN-CML029;

RX MEDLINE-99206606; PubMed-10192388;

RA Kalman S., Mitchell W., Marathe R.W., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.;

RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";

RL Nat. Genet. 21:385-389(1999).

RN 12

RP SEQUENCE FROM N.A.

RC STRAIN-AR39.

RX MEDLINE-20150255; PubMed-10684935;

RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey B.K., Peterson J., Uuterbach T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwin M., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;

RT "Genome sequences of Chlamydia trachomatis MOpn and Chlamydia pneumoniae AR39.";

RL Nucleic Acids Res. 28:1397-1406(2000).

RN 13

RP SEQUENCE FROM N.A.

RC STRAIN-J138.

RX MEDLINE-20330349; PubMed-10871362;

RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,

RA Shirai T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;

RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CML029 from USA.";

RL Nucleic Acids Res. 28:2311-2314(2000).

RN 14

RP SEQUENCE FROM N.A.

RC STRAIN-J138.

RX MEDLINE-20298986; PubMed-10839753;

RA Shirai M., Hirakawa H., Ouchi K., Tabuchi M., Kishi F., Kimoto M., Takeuchi H., Nishida J., Shibata K., Fujiwara R., Yoneda H., Matsushima H., Tanaka C., Furukawa S., Mura K., Nakazawa A., Ishii K., Shirai T., Hattori M., Kuhara S., Nakazawa T.;

RT "Comparison of outer membrane protein genes omp and pmp in the whole genome sequences of Chlamydia pneumoniae isolates from Japan and the United States.";

RL J. Infect. Dis. 181 Suppl 3:S524-S527(2000).

CC -1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES) (POTENTIAL).

CC -1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.

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CC EMBL: AE001638; AAD18679.1; -

DR EMBL: AE002181; AAF38083.1; -

DR EMBL: AP002547; BAA98745.1; -

DR HSSP: Q90121; 1KPT.

DR TIGR: CP0213; -

DR InterPro: IPR003368; Chlamydia_PMP.

DR InterPro: IPR003357; OMP.

DR Pfam: PF02385; OMP; 1.

DR Pfam: PF02415; DUF145; 1.

KW Outer membrane; Signal; Multigene family; Complete proteome.

FT SIGNAL 1 19

FT CHAIN 20 947

FT CONFLICT 453 453

FT E -> D (IN REF. 3).

SO SEQUENCE 947 AA; 103642 MW; 20CEIDEE1606DF CRC64;

Query Match 13.2%; Score 138; DB 1; Length 947;

Best local similarity 16.8%; Pred. No. 1 6e+02;

Matches 62; Conservative 29; Mismatches 69; Indels 210; Gaps 14;

QY 6 GTGYNNGYFYSY-----WMDGHGVTYNGPGQFSYWNMSNGNFYVGKGM 51

DB 600 GYGQGSWEFSWSPNDTKREKTTIASWT-----PTGFFSLDPRRSGFTPTTLM 648

QY 52 QGRTKKVYNFSG-----SYNPGNSYLS-----WSNPPLI 85

DB 649 S-----TFGSLNATISNIVNNVNNSEVYPLQHLGVFGGVYQIMQNPROSSNNLL 700

QY 86 EYIYENFGTYNP-----STGATKLGSEVTSQSYDIYRTQRVNQPSTIGATFYQYM 138

DB 701 VQHGHNVCARIPFSRNTLLSALTLQLFSSSSQONVADKSHAO-----ILIGTVSLNKSX 755

QY 139 ---SVR-----RNHRSSGSVNTA----- 153

DB 816 DLQYTKLVONPVENGYDPRFSSSEMTNLSPIGIALEMRFGSSSLQVSTSYIKD 875

QY 154 -----NHFNMAQOGLTGLG-----TMDQIYVAV-----EGYF 180

DB 876 LRRVNPQSSASLVLNHY-TWIDIOGVPLGKEALNTLNTLTIKTKIYVAWGISSTOREGSGN 934

QY 181 SSGSASITVS 190

Tue Jul 1 13:01:52 2003

us-09-990-874-16.rsp

Page 34

Db 935 LSANAHGLS 944

Search completed: July 1, 2003, 11:49:29
Job time : 17 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2003, 11:47:35 ; Search time 78 Seconds
(without alignments)
501.910 Million cell updates/sec

Title: US-09-990-874-16
Perfect score: 1045
Sequence: 1 OTIOPGTGNNCYFYSYND.....YQIVAVEGFSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	100.0	223	Q02244	002244 trichoderma
2	1033	98.9	223	Q09015	009015 trichoderma
3	876	83.8	223	Q090F9	Q090F9 trichoderma
4	767.8	73.5	241	Q12580	Q12580 chaetomium
5	705.9	67.6	219	Q12579	Q12579 chaetomium
6	702.5	67.2	232	Q09HEA4	Q09HEA4 aspergillus
7	696.9	66.7	290	Q09HEZ0	Q09HEZ0 phanerochaete
8	696.9	66.7	290	Q09HEY9	Q09HEY9 phanerochaete
9	688.5	65.9	295	Q09CIR2	Q09CIR2 fusarium ox
10	682.5	65.3	227	Q000263	Q000263 ascocochyta p
11	678.9	65.0	227	Q09UVZ3	Q09UVZ3 helminthosp
12	665.9	63.7	225	Q08TG22	Q08TG22 aspergillus
13	656.8	62.9	221	Q09UO2	Q09UO2 penicillium
14	647.9	62.0	223	Q09HFO	Q09HFO penicillium
15	635.9	60.9	231	Q13447	Q13447 cocillolobu
16	632.9	60.6	346	Q08VUT4	Q08VUT4 pseudomonas

17	631.3	60.4	221	3	P87037	P87037 aspergillus
18	628.9	60.2	231	3	Q00350	Q00350 cocillolobu
19	624.4	59.8	194	3	P81536	P81536 paecilomyce
20	615.9	58.7	227	3	Q09GEL	Q09GEL humicola gr
21	613.9	58.7	283	3	Q09UV7	Q09UV7 lentitula e
22	611	58.5	335	2	Q09OVB8	Q09OVB8 cellulomona
23	610.7	58.4	335	2	Q008346	Q008346 streptomyce
24	610.7	58.4	335	2	Q09RM44	Q09RM44 streptomyce
25	608.7	58.2	338	2	Q056265	Q056265 thermomono
26	606.9	58.1	231	3	Q09CIR1	Q09CIR1 fusarium ox
27	601.4	57.6	228	2	Q09962	Q09962 streptomyce
28	597.4	57.2	335	16	Q09KN6	Q09KN6 streptomyce
29	596.8	57.1	216	3	Q074716	Q074716 clavigeps p
30	594.5	56.9	329	2	Q09RMH9	Q09RMH9 streptomyce
31	568.6	54.4	191	2	Q09EH89	Q09EH89 streptomyce
32	540.9	51.8	661	2	Q056674	Q056674 pseudomonas
33	536.3	51.3	241	16	Q09R172	Q09R172 streptomyce
34	532.9	51.0	361	2	Q052375	Q052375 caldicellul
35	530.9	50.8	656	2	Q059300	Q059300 cellvibrio
36	528.9	50.6	360	2	P77853	P77853 dictyoglomu
37	527.4	50.5	240	2	Q056013	Q056013 streptomyce
38	527.3	50.5	210	16	Q09KEP3	Q09KEP3 bacillus ha
39	524	50.1	357	2	Q08VP72	Q08VP72 pseudomonas
40	518.3	49.6	211	2	Q043993	Q043993 aeromonas p
41	514.2	49.2	213	2	Q08VVC3	Q08VVC3 bacillus sp
42	509.7	48.8	213	2	Q09ZB36	Q09ZB36 bacillus su
43	506.2	48.4	213	2	Q059254	Q059254 bacillus su
44	505.2	48.3	213	2	Q059256	Q059256 bacillus sp
45	505	48.3	217	5	Q097402	Q097402 phaeodon coc

ALIGNMENTS

RESULT 1	Q002244	PRELIMINARY:	PRT:	223 AA.
ID	Q002244			
AC	Q002244:			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Endoxylanase II.			
GN	XLN2.			
OS	Trichoderma reesei (Hypocrea jecorina).			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocreales; Hypocreaceae; Hypocrea.			
OX	NCBI_TaxID=51453:			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:94088442; PubMed-8264524;			
RA	Saarelainen R., Paloheimo M., Fagerstrom R., Suominen P.L.,			
RA	Nevalainen K.M.;			
RT	"Cloning, sequencing and enhanced expression of the Trichoderma reesei			
RT	endoxylanase II (PI 9) gene xln2.";			
RL	Mol. Gen. Genet. 241:497-503(1993).			
DR	EMBL: S67387; AAB29346.1: -			
DR	HSSP: P36217; 1XVO.			
DR	InterPro: IPR001137; GH_11.			
DR	PIfam: PF00457; Glyco_hydro_11: 1.			
DR	PRINTS: PR00911; GLHYDRLASE11.			
DR	PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1: 1.			
DR	PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2: 1.			
KW	Glycosidase; Hydrolase; Xylan degradation.			
SO	SEQUENCE 223 AA; 24069 MW; 79668149EDAD22F9 CRC64;			
Query Match	100.0%; Score 1045; DB 3; Length 223;			
Best Local Similarity	100.0%; Pred. No. 5.1e-36;			
Matches 190; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
OY	1 OTIOPGTGNNCYFYSYNDGCGVYTTNGPGGFSYNNMNSGNGNYGCGMGPGRKNKYI 60			
DB				
	34 OTIOPGTGNNCYFYSYNDGCGVYTTNGPGGFSYNNMNSGNGNYGCGMGPGRKNKYI 93			

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QY 61 NFGSGYNPNNGNSLYSVGWSRNPFLIYIVENFGTYNPGTGAKLGEVTSDSGVYDIYRT 120
    |||||
DB 94 NFGSGYNPNNGNSLYSVGWSRNPFLIYIVENFGTYNPGTGAKLGEVTSDSGVYDIYRT 153
QY 121 QRVNPSIIGTATFTFYQWMSVRNRHRRSSGSVNTANHNMAAQQGLTGLTDYQIIVAVEGYF 180
    |||||
DB 154 QRVNPSIIGTATFTFYQWMSVRNRHRRSSGSVNTANHNMAAQQGLTGLTDYQIIVAVEGYF 213
QY 181 SSGSASITVS 190
    |||||
DB 214 SSGSASITVS 223

RESULT 2
099015 ID 099015 PRELIMINARY: PRT: 223 AA.
AC 099015:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Beta-xylanase precursor.
GN XYN2.
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-QM 6A.
RX MEDLINE-97076932; PubMed-8975597;
RA Grange D.C., Pretorius I.S., van Zyl W.H.;
RT "Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in
RT Saccharomyces cerevisiae."
RL Appl. Environ. Microbiol. 62:1036-1044(1996).
DR EMBL: U24191; AAB50278.1; -
DR HSSP: P36217; 1XVO.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 33
FT CHAIN 34 223
FT SEQUENCE 223 AA; 23981 MW; F696E545DAC90EB4 CRC64;

Query Match 98.9%; Score 1033; DB 3; Length 223;
Best local Similarity 98.9%; Pred. No. 1.6e-35;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTIQPGTYNGNGFYYSYVNDGHCQVYTYNGPGQSFVNMNSGPNFVGKGMOPGTKNKYI 60
    |||||
DB 34 QTIQPGTYNGNGFYYSYVNDGHCQVYTYNGPGQSFVNMNSGPNFVGKGMOPGTKNKYI 93
QY 61 NFGSGYNPNNGNSLYSVGWSRNPFLIYIVENFGTYNPGTGAKLGEVTSDSGVYDIYRT 120
    |||||
DB 94 NFGSGYNPNNGNSLYSVGWSRNPFLIYIVENFGTYNPGTGAKLGEVTSDSGVYDIYRT 153
QY 121 QRVNPSIIGTATFTFYQWMSVRNRHRRSSGSVNTANHNMAAQQGLTGLTDYQIIVAVEGYF 180
    |||||
DB 154 QRVNPSIIGTATFTFYQWMSVRNRHRRSSGSVNTANHNMAAQQGLTGLTDYQIIVAVEGYF 213
QY 181 SSGSASITVS 190
    |||||
DB 214 SSGSASITVS 223

RESULT 3
099VE9 ID 099VE9 PRELIMINARY: PRT: 223 AA.
AC 099VE9:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
```

```
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).
OS Trichoderma viride.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Mitosporic Hypocreales; Trichoderma.
OX NCBI_TaxID=5547;
RN [1]
RP SEQUENCE FROM N.A.
RA Furman-Matarasso N., Cohen E., Avni A.;
RT "Mutations in the Active Site of the Ethylene Inducing Xylanase
RT Elicitor Inhibits the b-1-4-Endoxylanase Activity but not the
RT Elicitation Activity."
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ012718; CAB60757.1; -
DR HSSP: P48793; 1XND.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 33
FT CHAIN 34 223
FT SEQUENCE 223 AA; 24230 MW; FBFB12028FB1212A CRC64;

Query Match 83.8%; Score 876; DB 3; Length 223;
Best local Similarity 82.1%; Pred. No. 4.7e-29;
Matches 156; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 1 QTIQPGTYNGNGFYYSYVNDGHCQVYTYNGPGQSFVNMNSGPNFVGKGMOPGTKNKYI 60
    |||||
DB 34 QTIQPGTYNGNGFYYSYVNDGHCQVYTYNGPGQSFVNMNSGPNFVGKGMOPGTKNKYI 93
QY 61 NFGSGYNPNNGNSLYSVGWSRNPFLIYIVENFGTYNPGTGAKLGEVTSDSGVYDIYRT 120
    |||||
DB 94 NFGSGYNPNNGNSLYSVGWSRNPFLIYIVENFGTYNPGTGAKLGEVTSDSGVYDIYRT 153
QY 121 QRVNPSIIGTATFTFYQWMSVRNRHRRSSGSVNTANHNMAAQQGLTGLTDYQIIVAVEGYF 180
    |||||
DB 154 QRVNPSIIGTATFTFYQWMSVRNRHRRSSGSVNTANHNMAAQQGLTGLTDYQIIVAVEGYF 213
QY 181 SSGSASITVS 190
    |||||
DB 214 SSGSASITVS 223

RESULT 4
012580 ID 012580 PRELIMINARY: PRT: 241 AA.
AC 012580:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Endo-beta-1,4-xylanase (EC 3.2.1.8).
GN CGXB.
OS Chaetomium gracile.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Chaetomiaceae; Chaetomium.
OX NCBI_TaxID=47794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96118924; PubMed-8595661;
RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
RT "Two family G xylanase genes from Chaetomium gracile and their
RT expression in Aspergillus nidulans."
RL Curr. Genet. 29:73-80(1995).
DR EMBL: D49851; BAA08650.1; -
DR HSSP: P36217; 1XVO.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
FT SIGNAL 1 33
FT CHAIN 34 223
FT SEQUENCE 241 AA; 25564 MW; DCD4B012272F77F CRC64;
```

Query Match 73.5%; Score 767.8; DB 3; Length 241;
Best Local Similarity 69.9%; Pred. No. 1.6e-24;
Matches 137; Conservative 21; Mismatches 26; Indels 12; Gaps 2;

OY 5 PG-----TCYNGCYFYSYWMDGCGVTTTNGPCGOFSSVNMNSGNGVGGKQWP 53
DB 25 PGMHRRQRLTSSQTGTNGCYYSFWTIDGQVNTNEAGQYVYMNGMNGVGGKQWP 84
OY 54 GTRKNVYFSGSYNPGNSVLSYVGSNRNPLEYIVENFGTYNPSTGATKLGVTSDGS 113
DB 85 GSA-RTINTANTNPNNGNSYLAIVGTRNPLEYIVENFGTYNPSTGATKLGVTSDGS 143
OY 114 VYDIYRTQVNPSTIGTATFYQVMSVRRNRSSGSVNTANHFNMAAQGLTGTMDYQI 173
DB 144 CYDIYRTQVNPSTIGTATFYQVMSVRRNRSSGSVNTANHFNMAAQGLTGTMDYQI 203
OY 174 VAVEGYFSSGSASTIV 189
DB 204 VATEGYSSGSATVNV 219

RESULT 5

ID 012579 PRELIMINARY: PRT; 219 AA.
AC 012579;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
GN Endo-beta1,4-xylanase A (EC 3.2.1.8).
OS Chaetomium gracile.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Chaetomiales; Chaetomium.
RN NCBI_TaxID=47794;
RX [1]
RP SEQUENCE FROM N.A.
RA MEDLINE:96118924; PubMed:8595661;
RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
RT "Two family G xylanase genes from Chaetomium gracile and their
RT expression in Aspergillus nidulans.";
RL Curr. Genet. 29:73-80(1995).
DR EMBL: D49850; BAA0849.1; -.
DR HSSP: P36217; 1XVO.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE1.
DR PROSITE: PS00776; GLYCOSTYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSTYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 219 AA; 23324 MW; 4729299E08FD9BA CRC64;

Query Match 67.6%; Score 705.9; DB 3; Length 219;
Best Local Similarity 68.1%; Pred. No. 4.6e-22;
Matches 126; Conservative 23; Mismatches 35; Indels 1; Gaps 1;

OY 6 GTGYNNGCYFYSWNDGCGVTTTNGPCGOFSSVNMNSGNGVGGKQWPCTKKKVINFSGS 65
DB 36 GTGTNNGCYFYSWNDGCGVTTTNGPCGOFSSVNMNSGNGVGGKQWPCTKKKVINFSGS 94
OY 66 YNPNGNSYLSYVGSNRNPLEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRTQVNP 125
DB 95 FSPGNGCYLAIVGTRNPLEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRTQVNP 154
OY 126 PSIIIGTATFYQVMSVRRNRSSGSVNTANHFNMAAQGLTGTMDYQIYAVGCTSSGSA 185
DB 155 PSIIIGTATFYQVMSVRRNRSSGSVNTANHFNMAAQGLTGTMDYQIYAVGCTSSGSA 214
OY 186 SITVS 190
DB 215 SITVS 219

RESULT 6

ID 09HFA4 PRELIMINARY: PRT; 232 AA.
AC 09HFA4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
GN xylanase G2 (EC 3.2.1.8).
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
RN NCBI_TaxID=5062;
RX [1]
RP SEQUENCE FROM N.A.
RA Kimura T., Sakka K., Ohmura K.;
RT "Molecular cloning, overexpression, and purification of major xylanase
RT from Aspergillus oryzae.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB044941; BAB20794.1; -.
DR HSSP: P36217; 1XVO.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE1.
DR PROSITE: PS00776; GLYCOSTYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSTYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 232 AA; 24605 MW; 1F73104751EA561C CRC64;

Query Match 67.2%; Score 702.5; DB 3; Length 232;
Best Local Similarity 59.7%; Pred. No. 7.1e-22;
Matches 126; Conservative 26; Mismatches 34; Indels 25; Gaps 2;

OY 3 IQP-----GTGYNNGCYFYSWNDGCGVTTTNGPCGOFSSV 38
DB 22 IEPLADHPNEAFNDAFNDLVGRSTPSSGTGYNNGCYFYSWNDGCGVTTTNGPCGOFSSV 81
OY 39 WNSGNGCYFYSWNDGCGVTTTNGPCGOFSSVNMNSGNGVGGKQWPCTKKKVINFSGS 98
DB 82 WNSGNGCYFYSWNDGCGVTTTNGPCGOFSSVNMNSGNGVGGKQWPCTKKKVINFSGS 140
OY 99 STGATKLGVTSDGSVYDIYRTQVNPSTIGTATFYQVMSVRRNRSSGSVNTANHFNA 158
DB 141 GSGGTATGCTTNTNHYQIYAVGCTSSGSAITV 200
OY 159 WAOGCTLTGTMDYQIYAVGCTSSGSAITV 189
DB 201 WAKYGLTGTNTNHYQIYAVGCTSSGSAITV 231

RESULT 7

ID 09HEZ0 PRELIMINARY: PRT; 290 AA.
AC 09HEZ0;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
GN Endo-1,4-B-xylanase B.
OS Phanerochaete chrysosporium.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Coriiciaceae; Phanerochaete.
RN NCBI_TaxID=5306;
RX [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ME446;
RA Khan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.;
RT "Molecular characterization and expression analysis of two endo-1,4-B-
RT xylanase genes from Phanerochaete chrysosporium.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF301904; AAG44994.1; -.
DR HSSP: P00725; 1A26.
DR InterPro: IPR000254; CBD_fungal.

RN [1]
RA SEQUENCE FROM N.A.
RP Kimura T., Sakka K., Ohmura K.;
RT "Acidophilic xylanase A from *Penicillium* sp. 40";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB035540; BAA86421.1; -.
DR HSSP: P36217; 1XTO.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 221 AA; 24171 MW; 98BDD5BCBEC860AD CRC64;

Query Match 62.9%; Score 656.8; DB 3; Length 221;
Best Local Similarity 61.8%; Pred. No. 5e-20;
Matches 118; Conservative 30; Mismatches 41; Indels 2; Gaps 2;

OY 1 QTIQPG-TCYNNGYRYSWNDGHCYVYTNPGGQFSYVMSNSGNFVGKGNQPGTKNKV 59
DB 32 QTISSQGTGNNGYSEFTNGCGTVQYTNCAAGEYVTWENCGDFTSGKMGSTGA-RD 90
OY 60 INFSGSYNPNNGSYLSYVGMNRNPLEYIVENFGTYPSTGATKLGVTSGSYVDIYR 119
DB 91 ITFEGTFNPSGNAYLAVGWTSPLEVEYILEDYCDYNGNSMTYKGTVSQGSVYDIYE 150
OY 120 TORVNPSTIGATFYQYVSVRRNRSSGSVNTANHFNAQAQGLTGTMDYQIYAVEGY 179
DB 151 HQQVNPSTIGATFYQYVSVRRNRSSGSVNTANHFNAQAQGLTGTMDYQIYAVEGY 210
OY 180 FSSGSASTIVS 190
DB 211 ESSGSSTIVS 221

RESULT 14

O9HFH0 PRELIMINARY; PRT: 223 AA.
AC O9HFH0;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Endo-1,4-xylanase precursor (EC 3.2.1.8).
GN XYN.
OS *Penicillium funiculosum*.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Penicillium*.
OX NCBI_TaxID=28572;
RN [1]
RP SEQUENCE FROM N.A.
RA Furniss C.S.M., Belshaw N.J., Alcocer M.J., Williamson G., Fish N.M.,
RT Kiron P.A.;
RT "Tight binding of a wheat xylanase inhibitor protein (XIP-1) to a
RT family 11 xylanase expressed homologically in *Penicillium*
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ278385; CAC15487.1; -.
DR HSSP: P36217; 1XTO.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1
FT CHAIN 34 223
FT SIGNAL 16
FT CHAIN 16
SQ SEQUENCE 223 AA; 24045 MW; 428CD224C8F13C77 CRC64;

Query Match 62.0%; Score 647.9; DB 3; Length 223;
Best Local Similarity 61.4%; Pred. No. 1.2e-19;
Matches 113; Conservative 29; Mismatches 41; Indels 1; Gaps 1;
OY 7 TCYNNGYRYSWNDGHCYVYTNPGGQFSYVMSNSGNFVGKGNQPGTKNKVINFSSY 66
DB 11 TCTNNGYRYSWNDGHCYVYTNPGGQFSYVMSNSGNFVGKGNQPGTKNKVINFSSY 66

DB 41 TCTNNGYRYSWNDGHCYVYTNPGGQFSYVMSNSGNFVGKGNQPGTKNKV 99
OY 67 NPNNGSYLSYVGMNRNPLEYIVENFGTYPSTGATKLGVTSGSYVDIYRTORVNP 126
DB 100 NPSGNAYLAVGWTSPLEVEYILEDYCDYNGNSMTYKGTVSQGSVYDIYRTORVNP 159
OY 127 STIGATFYQYVSVRRNRSSGSVNTANHFNAQAQGLTGTMDYQIYAVEGYFSSGSAS 186
DB 160 STEGSTSTNQVSVTERKRGVGTVTANHFNAQAQGLTGTMDYQIYAVEGYFSSGSST 219
OY 187 ITVS 190
DB 220 ITVS 223

RESULT 15

O13447 PRELIMINARY; PRT: 231 AA.
AC O13447;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Beta-1,4-xylanase.
GN XYL2.
OS *Cochliobolus sativus* (Bipolaris sorokiniana).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; *Cochliobolus*.
OX NCBI_TaxID=45130;
RN [1]
RP SEQUENCE FROM N.A.
RA Emami K., Hack E.;
RT "Characterisation of a xylanase gene from *Cochliobolus sativus* and its
RT expression.";
RL Mycol. Res. 0:0-0(0).
DR EMBL: AJ004802; CAA06151.1; -.
DR HSSP: O43097; 1YNA.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 231 AA; 25577 MW; 333E6DD1F065A6BF CRC64;

Query Match 60.9%; Score 635.9; DB 3; Length 231;
Best Local Similarity 59.3%; Pred. No. 3.9e-19;
Matches 112; Conservative 26; Mismatches 50; Indels 1; Gaps 1;

OY 1 QTIQPGTYNNGYRYSWNDGHCYVYTNPGGQFSYVMSNSGNFVGKGNQPGTKNKVI 60
DB 41 QTPSESEGYHNGCYFYSWMTDGGSAQYTMGGSRYSVTRNTGNFVGKGNPPT-GRVI 99
OY 61 NPSGSYNPNNGSYLSYVGMNRNPLEYIVENFGTYPSTGATKLGVTSGSYVDIYRT 120
DB 100 NYGAFNPNQNGYLAIVGWTSPLEVEYILEDYCDYNGNSMTYKGTVSQGSVYDIYRT 159
OY 121 QRVNPSTIGATFYQYVSVRRNRSSGSVNTANHFNAQAQGLTGTMDYQIYAVEGYF 180
DB 160 TRYNPSTIGATFYQYVSVRRNRSSGSVNTANHFNAQAQGLTGTMDYQIYAVEGYF 219

OY 181 SSGSASTIV 189
DB 220 SSGSASTIV 228

RESULT 16

O8VUT4 PRELIMINARY; PRT: 346 AA.
AC O8VUT4;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta-1,4-xylanase.

GN AYNA.
 OS Pseudomonas sp. ND137.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 NCBI_TaxID=147640;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ND137;
 RA Ackl Y., Kitamoto E., Myouga H., Kamel Y.;
 RT "Protoplast production of red alga Porphyra yezoensis by recombinant
 enzymes from Pseudomonas sp.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB063255; BAB79287.1; -
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; UNKNOWN_1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; UNKNOWN_1.
 KW Xylan degradation; Hydrolase; Glycosidase.
 SO SEQUENCE 346 AA; 36749 MW; F247F48FAF73B9E CRC64;

Query Match 60.6%; Score 632.9; DB 2; Length 346;
 Best Local Similarity 58.5%; Pred. No. 1.1e-18;
 Matches 107; Conservative 34; Mismatches 41; Indels 1; Gaps 1;
 QY 7 TGYNNGFYSYWMDGHGVYTNQPGGQFVSVMNSGNGFVGKGMQPTKKNKVINFGSY 66
 DB 32 TGTNNGFYTFWMDAPGTVMSTLGGSGNTGNTGVMGKGMNGGR-RIVSYSGTF 90
 QY 67 NPGNSYLSVYGSRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRTORVNP 126
 DB 91 NPGNGYLLTYGWTSPLEIYIYIDNMGSYRPGSGTYGTVMDGCTYDIYRTORVNP 150
 QY 127 SIITGATFYQYMSVRHRHSSGSVNTANHFMAAOCGLTGMDXQYVAVEGFSSGS 186
 DB 151 SIOTATFYQYMSVRROKRTGTTTGNHFDAMASHGLNHDYVMATGEGYSSGNSN 210
 QY 187 ITV 189
 DB 211 ITL 213

RESULT 17
 ID P87037 PRELIMINARY; PRT: 221 AA.
 AC P87037;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE XYNGL.
 GN XYNGL.
 OS Aspergillus oryzae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 NCBI_TaxID=5062;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KRN616;
 RA Kimura T., Kitamoto N., Kito Y., Karita S., Sakka K., Ohmura K.;
 RT "Cloning and sequence of xylanase G1 gene from Aspergillus oryzae
 KRN616.";
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB003085; BAA19744.1; -
 DR HSP: P36217; LYXO.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 SO SEQUENCE 221 AA; 23746 MW; C010E11E5F53C77E CRC64;

Query Match 60.4%; Score 631.3; DB 3; Length 221;
 Best Local Similarity 56.2%; Pred. No. 5.6e-19;
 Matches 113; Conservative 28; Mismatches 43; Indels 17; Gaps 2;

QY 5 PG-----TCYNNQFYSYWMDGHGVYTNQPGGQFVSVMNSGNGFVG 48
 DB 21 PGDSTLVELAKRAITSETGTNNGYYSFMTNGGDVEYIYNGNGQYSVAMTQNDNRVAG 80
 QY 49 KGMQPTKKNKVINFGSYNPNNGNSYLSVGSARNPLIEYIVENFGTYNPSTGATKLGCV 108
 DB 81 KGMNPGSA-KTVYTGSEMSNSYSVSLYGMTQNPLEVYIYDKYGDYDPTGATELGT 139
 QY 109 TSDGSVDIYRTQVRNQPSTIGATFYQYMSVRHRHSSGSVNTANHFMAAOCGLTGT 168
 DB 140 ESDGTYKIKYTRRNAPSIEGTSFNQYMSVRSGRVGGTITTAQNHFAMANYGLDGT 199
 QY 169 MDYQIVAVEGFSSGSASITV 189
 DB 200 HNYMILATFEGYKSSGSASITV 220

RESULT 18
 ID 000350 PRELIMINARY; PRT: 231 AA.
 AC 000350;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Xyl2 precursor.
 GN Xyl2.
 OS Cochliobolus carbonum (Bipolaris zeicola).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; Cochliobolus.
 NCBI_TaxID=5017;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SB113;
 RX MEDLINE=97055717; Pubmed=8900004;
 RA Abel-Birkhold P.C., Walton J.D.;
 RT "Cloning, disruption, and expression of two endo-beta 1,4-xylanase
 genes, XYL2 and XYL3, from Cochliobolus carbonum.";
 RL Appl. Environ. Microbiol. 62:4129-4135(1996).
 DR EMBL: U58915; AAC62815.1; -
 DR HSP: O43097; IYNA.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Signal.
 FT SIGNAL 41
 FT CHAIN 1
 FT CHAIN 41
 SO SEQUENCE 231 AA; 25576 MW; 237C3D49C4D0E871 CRC64;

Query Match 60.2%; Score 628.9; DB 3; Length 231;
 Best Local Similarity 58.7%; Pred. No. 7.6e-19;
 Matches 111; Conservative 26; Mismatches 51; Indels 1; Gaps 1;
 QY 1 OTIQPGTYNNGFYSYWMDGHGVYTNQPGGQFVSVMNSGNGFVGKGMQPTKKNKVI 60
 DB 41 OTSPSACGYHNGFYSMWTDGGSQAQYTMGEGSRVSTWRNTGNFVGKGMNPGS-GRVI 99
 QY 61 NFSGSYNPNNSYLSVYGSARNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVYDLYRT 120
 DB 100 NYGAFNPQNGYLAIVGWRNPLVEYVIESYCTVNPSSQAQKSGSFQPDGCTYNAVS 159
 QY 121 QRVNQPSTIGATFYQYMSVRHRHSSGSVNTANHFMAAOCGLTGTMDYQIVAVGCTF 180
 DB 160 TRYNOPTIDGTRFQYQYMSVTRORVGSVNMOMHFNAMSRYGGLNLDQHYQIVATGCTY 219
 QY 181 SSGSASITV 189
 DB 220 SSGSSDITV 228

RESULT 19

P81536 PRELIMINARY: PRT: 194 AA.

AC P81536: 01-JUN-2000 (TREMBlrel. 14, Created)

DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan xylanohydrolase) (PXY) (Fragment).

OS Paecilomyces variotii.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Paecilomyces.

OX NCBI_TaxID=45996;

RP X-RAY CRYSTALLOGRAPHY (1.59 ANGSTROMS), AND PARTIAL SEQUENCE.

RC STRAIN-BARNIER: MEDLINE=2009055; PubMed=10623548;

RA Kumar P.R., Bswaramoorthy S., Vilhathathil P.J., Vismamitra M.A.; "The tertiary structure at 1.59 Å resolution and the proposed amino acid sequence of a family-11 xylanase from the thermophilic fungus Paecilomyces variotii baltner";

RT J. Mol. Biol. 295:581-593(2000).

RU -1- CATALYTIC ACTIVITY: ENDOLYXOLYSIS OF 1,4-BETA-D-XYLOSIDIC LINKAGES IN XYLANS.

CC -1- PATHWAY: XYLAN DEGRADATION.

CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).

DR HSSP: 043097: 1YNA.

DR InterPro: IPR001137: GH_11.

DR Pfam: PF00457: Glyco_hydro_11: 1.

DR PRINTS: PR00911: GLHYDRASE11.

DR PROSITE: PS00776: GLYCOSYL_HYDROL_F11_1: 1.

DR PROSITE: PS00777: GLYCOSYL_HYDROL_F11_2: 1.

KW Xylan degradation: Hydrolase; Glycosidase; Acetylation.

FT MOD_RES 1 1

FT ACT_SITE 86 86 ACETYLATION.

FT ACT_SITE 178 178 NUCLEOPHILE (BY SIMILARITY).

FT DISULFD 110 154 PROTON DONOR (BY SIMILARITY).

FT NON_TER 194 194

SO SEQUENCE 194 AA; 20947 MW; 1D5C50AA4F6EDB90 CRC64;

Query Match 59.8%; Score 624.4; DB 3; Length 194;

Best Local Similarity 59.7%; Pred. No. 8.4e-19;

Matches 114; Conservative 26; Mismatches 45; Indels 6; Gaps 2;

QY 6 GT-----GYNNGYRYSYWNDSHGCVTYTNGPGGFSYVMSNSGNFVGKGNQPGTKNKVI 60

DB 1 GTTPNSGGMHDSGYYSWMSDGGDSTYTNNSGTYEITWNGMILVGKGNPGLNARAI 60

QY 61 NFSGSYNDNGNSYLSVGMRSNPLIEYIVENFGTYNPSTGATKLGVEYTSQGSYYDIYRT 120

DB 61 HFTVYTPNGTSTYLSVGMTRNPLVEYIVENFGSSNPSSTDLGTVSCGSGSTYTLGQS 120

QY 121 QRVNPSIIIGTATFYQYVSVRRNRHSSGSVNTANHFNMAAQGLTL-GTMDYQIVAVEGY 179

DB 121 TRVAPPSIDGTQTFNQVWSVRQDKRSSGTQVOTGCHFDAMASAGLVNVDHDTQIVATEGY 180

QY 180 FSSGSASITVS 190

DB 181 FSSGVARITVA 191

RESULT 20

O9HGEL PRELIMINARY: PRT: 227 AA.

AC O9HGEL: 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DE Beta-1,4-xylanase.

GN XYN2.

OS Humicola grisea var. thermoldea.

OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.

OX NCBI_TaxID=5528;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=60849;

RA Faria F.P., Pocas-Fonseca M.J., Azevedo M.O.; "Cloning of a xylanase-encoding gene from the thermophilic fungus Humicola grisea and its expression in Escherichia coli.";

RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RL EMBL: AF155594; AAG16891.1; -

DR HSSP: 043097: 1YNA.

DR InterPro: IPR001137: GH_11.

DR Pfam: PF00457: Glyco_hydro_11: 1.

DR PRINTS: PR00911: GLHYDRASE11.

DR PROSITE: PS00776: GLYCOSYL_HYDROL_F11_1: 1.

DR PROSITE: PS00777: GLYCOSYL_HYDROL_F11_2: 1.

KW Glycosidase; Hydrolase; Xylan degradation.

SO SEQUENCE 227 AA; 25615 MW; 991813AD8EB2939 CRC64;

Query Match 58.9%; Score 615.9; DB 3; Length 227;

Best Local Similarity 59.3%; Pred. No. 2.5e-18;

Matches 108; Conservative 25; Mismatches 48; Indels 1; Gaps 1;

QY 8 GYNNGEYSYWNDSHGCVTYTNGPGGFSYVMSNSGNFVGKGNQPGTKNKVINSGSYN 67

DB 44 GWHNGEYSYWNDSHGCVTYTNGPGGFSYVMSNSGNFVGKGNQPGTKNKVINSGSYN 102

QY 68 PNGNSYLSVGMRSNPLIEYIVENFGTYNPSTGATKLGVEYTSQGSYYDIYRTQVNPNS 127

DB 103 PNGNGYLAIVGWTNPLVEYIVESGYTNGPGGFSYVMSNSGNFVGKGNQPGTKNKVINSGSYN 162

QY 128 IIGTATFYQYVSVRRNRHSSGSVNTANHFNMAAQGLTLGTMDOYIVAVEGYFSSGSASI 187

DB 163 IDGRTFOQYVSVRRNRHSSGSVNTANHFNMAAQGLTLGTMDOYIVAVEGYFSSGSASI 222

QY 188 TV 189

DB 223 YV 224

RESULT 21

O96UV7 PRELIMINARY: PRT: 283 AA.

AC O96UV7: 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DE Xylanase.

GN XYN11A.

OS Lentinula edodes (Shiitake mushroom) (Lentinus edodes).

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

OC Agaricales; Tricholomataceae; Lentinula.

OX NCBI_TaxID=5353;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=STAMETS CS-2;

RA Lee C.C., Wong D.W.S., Robertson G.H.; "Cloning and characterization of xylanase (xyn11A) from Lentinula edodes.";

RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL: AF411252: AAL04152.1; -

DR InterPro: IPR000254: CBD_Fungal.

DR InterPro: IPR001137: GH_11.

DR Pfam: PF00734: CBM_1: 1.

DR Pfam: PF00457: Glyco_hydro_11: 1.

DR ProDom: PD001821: CBD_Fungal: 1.

DR PROSITE: PS00562: CBD_FUNGAL: 1.

DR PROSITE: PS00777: GLYCOSYL_HYDROL_F11_2: UNKNOWN_1.

SO SEQUENCE 283 AA; 29474 MW; A41B94A7F8677243 CRC64;

Query Match 58.7%; Score 613.9; DB 3; Length 283;

Best Local Similarity 58.7%; Pred. No. 4.6e-18;

Matches 111; Conservative 26; Mismatches 51; Indels 1; Gaps 1;


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OY 1 QTIOPGTGNYNGFYFSYVNDHGQVYTYNGPGQGFVSVMNSNGNFVGKGMQPGTKNKYI 60
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 32 RSIPNGEFGNNNGFYFSVSDTIVTGTGTGPGGEGTLLTGSGSDVYVGGMPPGGMMSV - 90
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 61 NMSGYNPNPNSYLSYVGMNRNPLEYIVENFGYINPSTGATKLGEXTSDGSVDIYRT 120
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 91 EYSGYSPNGNSYLSYVGMNTPLEVEYITDSFGDVPNPTSGTGLCTCTSDGVDIYRTQ 150
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 121 QVNOPSTIIGTATFQYVMSVRNRHSSGSVNTANHFNMAAQGLTGTMDOIVANEGYF 180
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 151 TTRMAPSIGTATFQYVMSIRQTHRVGGTGTGNGHSCWESVGLPLGTFTNYITLATEGYS 210
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 181 SSGSASITV 189
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 211 SSGTSTITV 219
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 22
O9ROB8 PRELIMINARY: PRT: 335 AA.
AC 09ROB8:
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Endo-1,4-beta-xylanase (EC 3.2.1.8).
GN XYN1A.
OS Cellulomonas pachnodae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae.
OC Actinomycetales; Micrococcales; Cellulomonadales; Cellulomonas.
OX NCBI_TaxID=101489;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99402756; PubMed=10473422;
RT "Molecular and biochemical characterization of two xylanase-encoding
genes from Cellulomonas pachnodae."
RL Appl. Environ. Microbiol. 65:4099-4107(1999).
DR EMBL: AF120156; AAD54767.1;
DR HSP: P09850; 1XNB.
DR InterPro: IPR001919; Bac_cellose-bind.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00553; CBM_2; 1.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 335 AA; 34383 MW; 64EFD808C25542D CRC64;

Query Match
Best Local Similarity 58.5%; Score 611; DB 2; Length 335;
Matches 109; Conservative 32; Mismatches 42; Indels 10; Gaps 3;

OY 4 QP-----GTGYNNGFYFSYVNDHGQVYTYNGPGQGFVSVMNSNGNFVGKGMQPGTK 56
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 40 QPAAVDSNSTSGSGFYFWTDAPGTYSMNLGSGGNSYTSMSNTGNFVAGKMGTSASA 99
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 57 NKVINSSGSYNPNPNSYLSYVGMNRNPLEYIVENFGYINPSTGATKLGEXTSDGSVD 116
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 100 -PTISTSGFNPSGNAYLAVYVMSHDPLEVEYIVDSWGTGTRPT--GTFMGTVNSDGTAD 156
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 117 IYRTQVNOPSTIIGTATFQYVMSVRNRHSSGSVNTANHFNMAAQGLTGTMDOIVAV 176
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 157 IYKTRTMAPSIGTATFQYVMSVRNSKRVGTTITANHFNMAASHGMNLGRHDYIAT 216
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 177 EGYFSSGSASITV 189
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 217 EGYSSGSSSNITI 229
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 23
O08346 PRELIMINARY: PRT: 335 AA.
ID 008346
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AC 008346:
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Xylanase precursor (EC 3.2.1.8).
GN STX11.
OS Streptomyces thermoviolaceus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae.
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1952;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OPC-520;
RX MEDLINE=97176398; PubMed=9023944;
RA Tsujibo H., Ohtsuki T., Iio T., Yamazaki I., Miyamoto K., Sugiyama M.,
  Inamori Y.
RT "Cloning and sequence analysis of genes encoding xylanases and
acetylxyylan esterase from Streptomyces thermoviolaceus OPC-520."
RL Appl. Environ. Microbiol. 63:661-664(1997).
DR EMBL: D85897; BAA19778.1;
DR HSP: P09850; 1XNB.
DR InterPro: IPR001919; Bac_cellose-bind.
DR InterPro: IPR001137; GH_11.
DR InterPro: IPR001230; Prenyl_site.
DR Pfam: PF00553; CBM_2; 1.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR PROSITE: PS00294; PRENYLATION; UNKNOWN_1.
KM Glycosidase; Hydrolase; Signal.
FT SIGNAL 1
SQ SEQUENCE 335 AA; 35280 MW; B9C9AA0C2BA0241 CRC64;

Query Match
Best Local Similarity 58.4%; Score 610.7; DB 2; Length 335;
Matches 109; Conservative 28; Mismatches 43; Indels 3; Gaps 3;

OY 7 TGYNNGFYFSYVNDHGQVYTYNGPGQGFVSVMNSNGNFVGKGMQPGTKNKVINFSGSY 66
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 48 TGTNNGFYFSFWTDAPGTVMNTGAGGNSYTSMSNTGNFVAGKMGATGGR-RTVYSSGTF 106
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 67 NPNGSYLSYVGMNRNPLEYIVENFGYINPSTGATKLGEXTSDGSVDIYRTQVNOP 126
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 107 NMSGAYLALYGMNSQNPLEVEYIVDSWGTGTRPT--GTGYSDGCTDIYMTIRYANP 164
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 127 STIGTATFQYVMSVRNRHSSGSVNTANHFNMAAQGLTGTMDOIVAVEGYFSSGSAS 186
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 165 STIEGTFEQYVMSVRNKRRTGTTTGNHFDMAAHGMPLGTFPNWIIATEGYSSGSSN 224
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 187 ITV 189
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 225 ITV 227
    ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 24
O9RMM4 PRELIMINARY: PRT: 335 AA.
ID O9RMM4:
AC 09RMM4:
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Xylanase B precursor.
GN XYNB.
OS Streptomyces thermocyanoviolaceus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae.
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=106355;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KCCM 40049;
RA Shin J.-H., Choi J.-H., Lee O.-S., Joo G.-J., Rhae I.-K.;
  "Streptomyces thermocyanoviolaceus xynB (xylanase B).";
```

R	L	Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
DR	EMBL:	AFL194025; AAF04601.1; -
DR	HSSP:	P09850; 1XNB.
DR	InterPro:	IIPR001919; Bac_celose-bind.
DR	InterPro:	IIPR001137; GH_11.
DR	InterPro:	IIPR001230; Prenyl_site.
DR	pfam:	PF00553; CBM_2; 1.
DR	pfam:	PF00457; Glyco_hydro_11; 1.
DR	PRINTS:	PR00911; GLYDRLASE1.
DR	PROSITE:	PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR	PROSITE:	PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW	SIGNAL:	-
FT	CHAIN	1 POTENTIAL.
SO	SEQUENCE	335 AA; 35328 MW; D/DED/BACBS2710 CRC64;
OY	Query Match	58.4%; Score 610.7; DB 2; Length 335;
Dd	Best Local Similarity	59.6%; Pred. No. 8,7e-18;
	Matches 109; Conservative	28; Mismatches 43; Indels 3; Gaps 3
OY	7	TGYNNGIYSYWNDHGCVITYTNGPGQGYFVSNWSNMGFVGKGMQPCKKKVINFGSGY 66
Dd	48	TGFHNGIYSFWTDAPCGTVMTAGAGGVSTQMSNTGNFVAGKGATGCR-RIVYISGTF 106
OY	67	NPNQNSLYSVYGWGRNPILERYIYEENFGTYNPSGTATLGVTSPDGSYDYDIYRQRVNQP 126
Dd	107	NPSGAAYATALGWSONPLVEYYIYIDNMGTYP-R-TGYI-GTVYSDGGTYDIYMTTRYMAP 164
OY	127	SIIGTAPEYQQYQWVSRRNRHSRGSVYANTAHFNAMAQOGTLTGMDYOIVAEGVFSSGSAS 186
Dd	165	SIEGKTPTNOYWSVRQNKRTGCTITTCNHFPDAMAHGMPLTGFNTMIATEGYQSSGSSN 224
OY	187	ITV 189
Dd	225	ITV 227
RESULT 25		
ID	056265	PRELIMINARY; PRT; 338 AA.
AC	056265;	
DT	01-NOV-1996	(TREMBLrel. 01, Created)
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)
DE	Endo 1,4-beta-D-xylanase precursor.	
GN	TPXA.	
OS	Thermomonospora fusca.	
OC	Bacteria; Firmicutes; Actinobacteriæ; Actinobacteridae;	
CC	Actinomycetales; Streptosporangineae; Nocardiopsaceae; Thermofilida.	
OX	NCBI_Taxid=2021;	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-YX:	
RC	MEDLINE=94213454; PubMed=8161173;	
RA	Irwin D., Jung E.D., Wilson D.B.;	
RT	"Characterization and sequence of a Thermomonospora fusca xylanase.";	
RL	Appl. Environ. Microbiol. 60:763-770(1994).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-YX:	
RC	MEDLINE=89255048; Pubmed=2656632;	
RA	Ghangas G.S., Hu Y.J., Wilson D.B.;	
RT	"Cloning of a Thermomonospora fusca xylanase gene and its expression	
RL	in Escherichia coli and Streptomyces lividans.";	
JL	J. Bacteriol. 171:2963-2969(1989).	
DR	EMBL: U01242; AAA21480.1; -	
DR	HSSP: P09850; 1XNB.	
DR	InterPro: IIPR001137; GH_11.	
DR	pfam: PF00457; Glyco_hydro_11; 1.	
DR	PRINTS: PR00911; GLYDRLASE1.	
DR	PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.	
DR	PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.	

[illegible]

OC Eukaryote: Fungi: Ascomycota: Pezizomycotina: Sordariomycetes;
 OC Hypocreales: Clavicipitaceae: Claviceps.
 OC NCBI_TaxID=5111;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=75:
 RA Giesbert S., Lepping H.B., Tenberge K.B., Tudzynski P.;
 RT "The xylanolytic system of *Claviceps purpurea*: cytological evidence
 for secretion of xylanases in infected rye tissue and molecular
 characterization of two xylanase genes.";
 RL Phytopathology 88:1020-1030(1998).
 DR EMBL: Y16969; CAA76570.1; -
 DR HSP: P36217; IXYO.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 KW Glycosidase: Hydrolase: Signal; Xylan degradation.
 FT SIGNAL
 FT SEQUENCE 216 AA; 23339 MW; 012E874E939E7581 CRC64;

Query Match 57.1%; Score 596.8; DB 3; Length 216;
 Best Local Similarity 58.2%; Pred. No. 1.4e-17;
 Matches 106; Conservative 29; Mismatches 45; Indels 2; Gaps 2;

QY 9 YNNGEYFYSYVNDHGVTYNGPGQFVSVMNSGNEFVGKGNQPGTKNKVINFGSGYNP 68
 ID 09RMH9 PRELIMINARY; PRT; 329 AA.
 AC 09RMH9;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Xylanase.
 GN SVXA.
 OS Streptomyces viridosporus.
 OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
 OC Actinomycetales: Streptomycinae: Streptomycetaceae: Streptomyces.
 OC NCBI_TaxID=67581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=77A;
 RA Kanhiyur D.N., Magnuson T.S., Crawford D.L.;
 RT "Cloning, sequencing and characterization of the xylanase-encoding
 RT gene svxa, from *Streptomyces viridosporus* T7A, and its expression in
 RT *Escherichia coli*.";
 RL Nippon Hosenkin Gakkaishi 0:0-0(2000).
 DR EMBL: AF198618; AAF09501.1; -
 DR HSP: P09850; IXNB.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR PROSITE: PS00294; PRENYLATION; UNKNOWN.1
 SO SEQUENCE 329 AA; 35132 MW; 7E9C7A625664E637 CRC64;

RESULT 30

Q9RMH9 PRELIMINARY; PRT; 329 AA.
 ID 09RMH9;
 AC 09RMH9;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Xylanase.
 GN SVXA.
 OS Streptomyces viridosporus.
 OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
 OC Actinomycetales: Streptomycinae: Streptomycetaceae: Streptomyces.
 OC NCBI_TaxID=67581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=77A;
 RA Kanhiyur D.N., Magnuson T.S., Crawford D.L.;
 RT "Cloning, sequencing and characterization of the xylanase-encoding
 RT gene svxa, from *Streptomyces viridosporus* T7A, and its expression in
 RT *Escherichia coli*.";
 RL Nippon Hosenkin Gakkaishi 0:0-0(2000).
 DR EMBL: AF198618; AAF09501.1; -
 DR HSP: P09850; IXNB.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR PROSITE: PS00294; PRENYLATION; UNKNOWN.1
 SO SEQUENCE 329 AA; 35132 MW; 7E9C7A625664E637 CRC64;

Query Match 56.9%; Score 594.5; DB 2; Length 329;
 Best Local Similarity 54.5%; Pred. No. 3.9e-17;
 Matches 108; Conservative 32; Mismatches 43; Indels 15; Gaps 4;

QY 5 PGT-----GYNNGEYFYSYVNDHGVTYNGPGQFVSVMNSGNEFVGKGNQ 52
 ID 09EM89 PRELIMINARY; PRT; 191 AA.
 AC 09EM89;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Beta-xylanase (EC 3.2.1.8) (Fragment).
 GN GXYN.
 OS Streptomyces olivaceoviridis (Streptomyces corchorusii).
 OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
 OC Actinomycetales: Streptomycinae: Streptomycetaceae: Streptomyces.
 OC NCBI_TaxID=1921;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-86;
 RA Bin Y.;
 RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-86;
 RA Zhang H., Yao B., Wang Y.;
 RT "Cloning and expression of the 23kd beta-xylanase gene from
 RT Streptomyces olivaceoviridis E-86.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A2929217; CAC19491.1; -
 DR HSP: P09850; IXNB.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Glycosidase: Hydrolase: Xylan degradation.
 FT NON_TER
 FT SEQUENCE 191 AA; 20781 MW; 7E1C45AADE1B6B9C CRC64;

RESULT 31

Q9EM89 PRELIMINARY; PRT; 191 AA.
 ID 09EM89;
 AC 09EM89;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Beta-xylanase (EC 3.2.1.8) (Fragment).
 GN GXYN.
 OS Streptomyces olivaceoviridis (Streptomyces corchorusii).
 OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
 OC Actinomycetales: Streptomycinae: Streptomycetaceae: Streptomyces.
 OC NCBI_TaxID=1921;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-86;
 RA Bin Y.;
 RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-86;
 RA Zhang H., Yao B., Wang Y.;
 RT "Cloning and expression of the 23kd beta-xylanase gene from
 RT Streptomyces olivaceoviridis E-86.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A2929217; CAC19491.1; -
 DR HSP: P09850; IXNB.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Glycosidase: Hydrolase: Xylan degradation.
 FT NON_TER
 FT SEQUENCE 191 AA; 20781 MW; 7E1C45AADE1B6B9C CRC64;

Query Match 54.4%; Score 568.6; DB 2; Length 191;
 Best Local Similarity 55.1%; Pred. No. 1.6e-16;
 Matches 102; Conservative 32; Mismatches 47; Indels 4; Gaps 4;

QY 7 TGYNNGEYFYSYVNDHGVTYNGPGQFVSVMNSGNEFVGKGNQPGTKNKVINFGSGY 66
 ID 09EM89 PRELIMINARY; PRT; 191 AA.
 AC 09EM89;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Beta-xylanase (EC 3.2.1.8) (Fragment).
 GN GXYN.
 OS Streptomyces olivaceoviridis (Streptomyces corchorusii).
 OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
 OC Actinomycetales: Streptomycinae: Streptomycetaceae: Streptomyces.
 OC NCBI_TaxID=1921;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-86;
 RA Bin Y.;
 RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-86;
 RA Zhang H., Yao B., Wang Y.;
 RT "Cloning and expression of the 23kd beta-xylanase gene from
 RT Streptomyces olivaceoviridis E-86.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A2929217; CAC19491.1; -
 DR HSP: P09850; IXNB.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Glycosidase: Hydrolase: Xylan degradation.
 FT NON_TER
 FT SEQUENCE 191 AA; 20781 MW; 7E1C45AADE1B6B9C CRC64;

QY 9 TGTNNNGEYFYSYVNDHGVTYNGPGQFVSVMNSGNEFVGKGNQPGTKNKVINFGSGY 67
 ID 09EM89 PRELIMINARY; PRT; 191 AA.
 AC 09EM89;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Beta-xylanase (EC 3.2.1.8) (Fragment).
 GN GXYN.
 OS Streptomyces olivaceoviridis (Streptomyces corchorusii).
 OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
 OC Actinomycetales: Streptomycinae: Streptomycetaceae: Streptomyces.
 OC NCBI_TaxID=1921;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-86;
 RA Bin Y.;
 RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-86;
 RA Zhang H., Yao B., Wang Y.;
 RT "Cloning and expression of the 23kd beta-xylanase gene from
 RT Streptomyces olivaceoviridis E-86.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A2929217; CAC19491.1; -
 DR HSP: P09850; IXNB.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Glycosidase: Hydrolase: Xylan degradation.
 FT NON_TER
 FT SEQUENCE 191 AA; 20781 MW; 7E1C45AADE1B6B9C CRC64;

QY 67 NPNGNSYLSVYGWSRNPFLIEYIVENFGTYNPGTATKLGTYSDGSVYDIYRTORVNP 126
 ID 09EM89 PRELIMINARY; PRT; 191 AA.
 AC 09EM89;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Beta-xylanase (EC 3.2.1.8) (Fragment).
 GN GXYN.
 OS Streptomyces olivaceoviridis (Streptomyces corchorusii).
 OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
 OC Actinomycetales: Streptomycinae: Streptomycetaceae: Streptomyces.
 OC NCBI_TaxID=1921;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-86;
 RA Bin Y.;
 RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-86;
 RA Zhang H., Yao B., Wang Y.;
 RT "Cloning and expression of the 23kd beta-xylanase gene from
 RT Streptomyces olivaceoviridis E-86.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A2929217; CAC19491.1; -
 DR HSP: P09850; IXNB.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Glycosidase: Hydrolase: Xylan degradation.
 FT NON_TER
 FT SEQUENCE 191 AA; 20781 MW; 7E1C45AADE1B6B9C CRC64;

QY 68 YPSGNGYALALYGMTSNPLIEYIVDMWGVYRP-TGYK-GTYSGGCTDYVQTRYNAP 125
 ID 09EM89 PRELIMINARY; PRT; 191 AA.
 AC 09EM89;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Beta-xylanase (EC 3.2.1.8) (Fragment).
 GN GXYN.
 OS Streptomyces olivaceoviridis (Streptomyces corchorusii).
 OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
 OC Actinomycetales: Streptomycinae: Streptomycetaceae: Streptomyces.
 OC NCBI_TaxID=1921;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-86;
 RA Bin Y.;
 RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-86;
 RA Zhang H., Yao B., Wang Y.;
 RT "Cloning and expression of the 23kd beta-xylanase gene from
 RT Streptomyces olivaceoviridis E-86.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A2929217; CAC19491.1; -
 DR HSP: P09850; IXNB.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Glycosidase: Hydrolase: Xylan degradation.
 FT NON_TER
 FT SEQUENCE 191 AA; 20781 MW; 7E1C45AADE1B6B9C CRC64;

QY 127 SLTGATTFQYQSVYRNHSSGVSNTANFNMAAQQGLTGMDO-YQYAVGCTFSSGSA 185
 ID 09EM89 PRELIMINARY; PRT; 191 AA.
 AC 09EM89;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Beta-xylanase (EC 3.2.1.8) (Fragment).
 GN GXYN.
 OS Streptomyces olivaceoviridis (Streptomyces corchorusii).
 OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
 OC Actinomycetales: Streptomycinae: Streptomycetaceae: Streptomyces.
 OC NCBI_TaxID=1921;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-86;
 RA Bin Y.;
 RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-86;
 RA Zhang H., Yao B., Wang Y.;
 RT "Cloning and expression of the 23kd beta-xylanase gene from
 RT Streptomyces olivaceoviridis E-86.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A2929217; CAC19491.1; -
 DR HSP: P09850; IXNB.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Glycosidase: Hydrolase: Xylan degradation.
 FT NON_TER
 FT SEQUENCE 191 AA; 20781 MW; 7E1C45AADE1B6B9C CRC64;

QY 126 SVEGKTFNQYQSVYRNHSSGVSNTANFNMAAQQGLTGMDO-YQYAVGCTFSSGSA 185
 ID 09EM89 PRELIMINARY; PRT; 191 AA.
 AC 09EM89;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Beta-xylanase (EC 3.2.1.8) (Fragment).
 GN GXYN.
 OS Streptomyces olivaceoviridis (Streptomyces corchorusii).
 OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
 OC Actinomycetales: Streptomycinae: Streptomycetaceae: Streptomyces.
 OC NCBI_TaxID=1921;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-86;
 RA Bin Y.;
 RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-86;
 RA Zhang H., Yao B., Wang Y.;
 RT "Cloning and expression of the 23kd beta-xylanase gene from
 RT Streptomyces olivaceoviridis E-86.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A2929217; CAC19491.1; -
 DR HSP: P09850; IXNB.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Glycosidase: Hydrolase: Xylan degradation.
 FT NON_TER
 FT SEQUENCE 191 AA; 20781 MW; 7E1C45AADE1B6B9C CRC64;

OY		186	SITVS	190	-	
DB		186	NITVS	190		
 RESULT 32						
ID	059674	.	PRELIMINARY:	PRT:	661 AA.	
AC	059674:					
DT	01-NOV-1996	(TREMblrel_01, Created)				
DT	01-NOV-1996	(TREMblrel_01, last sequence update)				
DT	01-JUN-2002	(TREMblrel_21, last annotation update)				
DE	Endo-beta-1,4-xylanase (EC 3.2.1.8).					
OS	Pseudomonas fluorescens.					
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;					
OX	Pseudomonas.					
RN	NCBI_TaxID=294;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=CELLULOSA;					
RX	MEDLINE=96077124; PubMed=7492333;					
RA	Millward-Sadler S.J., Davidson K., Hazlewood G.P., Black G.W.,					
RA	Gilbert H.J., Clarke J.H.;					
RT	"Novel cellulose-binding domains, NoB homologues and conserved					
RT	modular architecture in xylanases from the aerobic soil bacteria					
RL	Pseudomonas fluorescens subsp. cellulosa and Cellvibrio mixtus.",					
BL	Biochem. J. 312:39-48(1995);					
DR	EMBL; Z48927; CAA8763.1; -;					
DR	HSSP; P36217; 1XO.					
DR	InterPro: IPR002883; CBD_5.					
DR	InterPro: IPR001137; GH_11.					
DR	InterPro: IPR002509; Polysac_deacet.					
DR	Pfam; PF02013; CBM_10; 1.					
DR	Pfam; PF00457; Glyco_hydro_11; 1.					
DR	Pfam; PF01522; Polysac_deacet; 1.					
DR	PRINTS; PR00911; GLHYDRLASE11.					
KW	PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.					
SO	Glycosidase; Hydrolase; xylan degradation.					
SEQUENCE	661 AA: 69193 MW; 38C897D4C732FEB CRC64;					
 Query Match 51.8%; Score 540.9; DB 2; Length 661; Best Local Similarity 51.0%; Pred. No. 2,4e-14; Matches 102; Conservative 39; Mismatches 48; Indels 11; Gaps 6						
OY	1 OTIQD-GICGYNNGIYYTYWINDGHGGVTTTNGFGQFVSNWSNS-GNFVGKGMDPGTKNK	58				
DB	28 QTLSSNSTGTCTNNGFYTWMKDS-GDASMTLLSGCRYOSMGNSTNNVOCKGMNDGNNSR	86				
OY	59 VINFSGSY--NPNGNSLYSVYGMSRNPLIEYIVENFGTVNPS--TGATTKIGEVTSDGSV	114				
DB	87 VISISGSIQVDSSONSYSIALIGWTISPLETEIVIESYGYNPAVSCSGGTDYDFSDGDAT	146				
OY	115 YDIYRTQRPVNPSIIINGTAFYQYVMSVRNRHRS---SGSVNTANFNMAAQGLTLGTMID	170				
DB	147 YNVRCRGVPNQPSIDGTQTFQYFESVRPKKGFNGINSGITFPANNVNEFWASGILNLGRHN	206				
OY	171 VOIYAVEGEIFSSGSASTVS 190					
DB	207 YOVIATEGYRGSSSDITS 226					
 RESULT 33						
ID	09R172	.	PRELIMINARY:	PRT:	241 AA.	
AC	09R172:					
DT	01-MAY-2000	(TREMblrel_13, Created)				
DT	01-MAY-2000	(TREMblrel_13, last sequence update)				
DT	01-JUN-2002	(TREMblrel_21, last annotation update)				
DE	Endo-1,4-beta-xylanase.					
CN	XLMC OR SCO0105 OR SCJ11.34C.					
OC	Streptomyces coelicolor.					
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;					

Query Match	Best Local Similarity	Score	51.3%	DB 16	Length 241:
Matches	100: Conservative	34:	Mismatches	49:	Indels 17: Gaps 6
QY	5	POTGY	-----	NGGYFYSYVNDHGAGVYTNNGPGGQFSSVNMNSGNEFGGKQMP	53
DB	44	PCTAAATTTTNGTGTCDGDMYSSFWMTDGGGVSMTLNGGGSYSTQGTNCGNFVAGKQWST	103		
QY	54	GTKNNVINFSGSYNNGNSYLSVYGMSRNPLEIYIVENFGYTNPNSTGATKLCLEVISDS	113		
DB	104	GGR-FTVRRNGFVNSGNGGCGGLGWTSPNPLEYIIVDMWGSYRP-TGTYYK-GTVSSDDG	160		
QY	114	VYDIPTRVQNPSSLIGTATFQVQYSVRRNRHSSGGS--VNTANHFENAMAOQGLTGTM-D	170		
DB	161	TYDIQTTRYNAPSVEGTKTKTPQOQYVSVYRSKVTSSGGLTTTGNHFDAMARACGNMQQFRT	220		
QY	171	YQIYAVEGTFSSGASATVS	190		
DB	221	YIMATGEGYSSGSSNITVS	240		
RESULT	34				
OS2375					
ID	052375	PRELIMINARY:	PRT:	361	AA.
AC	052375:				
DT	01-JUN-1998 (TREMBLrel. 06, created)				
DT	01-JUN-1998 (TREMBLrel. 06, last sequence update)				


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OY      180 FSSGSASIT 188
        11111:11
Db      211 QSSGSANIT 219

RESULT 37
O56013
ID      056013      PRELIMINARY;      PRT;      240 AA.
AC      056013:
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE      Xylanase precursor.
OS      Streptomyces sp. EC3.
OC      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC      Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX      NCBI_TaxID=99388;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-EC3;
RX      MEDLINE=96293859; PubMed=8722569;
RT      Mazy-Servais C., Moreau A., Gerard C., Dusart J.;
RT      "Cloning and sequencing of a xylanase-encoding gene from Streptomyces
RT      sp. EC3."?;
RL      DNA Seq. 6:147-158(1996).
DR      EMBL: X81045; CAA56935.1; -
DR      HSSP: P09850; 1XNB.
DR      InterPro: IPR001137; GH_11.
DR      Pfam: PF00457; Glyco_hydro_11; 1.
DR      PRINTS: PR00911; GLHYDLASE11.
DR      PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR      PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM      Signal.
FT      SIGNAL.      1      49      POTENTIAL.
FT      CHAIN      50      240      XYLANASE.
SQ      SEQUENCE      240 AA; 25949 MW; 5D0B864A4497FC33 CRC64;

Query Match      50.5%; Score 527.4; DB 2; Length 240;
Best Local Similarity 53.8%; Pred. No. 1.2e-14;
Matches 100; Conservative 31; Mismatches 49; Indels 6; Gaps 6;

OY      7 TGYNNGFYSYWMDHGGVTTYTNGPGQSFVNSNSGNEFVGKGMQPGTKNKVINFSGSY 66
        11111:11111:11111:11111:11111:11111:11111:11111:11111:11111:
Db      58 TGY-DCMYSGFMWDGGGVSVMTLNNGSGSYTQMTNCGNFYAGKMGNGGR-RIVRYSGYF 115

OY      67 NPGNSLSTLYSGSRNPLEYIVENFGTYNPSTGATKLGCVTSDSGVYDITQRYVNOP 126
        11111:11111:11111:11111:11111:11111:11111:11111:11111:11111:
Db      116 NPGNGSGCLYGTWSNPLVEYIYDMNGSYRP-TGEYR-GTVYSDGGTYDIYKTRYNAP 173

OY      127 SIIGTATFYQYWSVRRNH-RSSGSVNTANHFENMAAOGLTGTMD-VQIVAVEGYSFGS 184
        11111:11111:11111:11111:11111:11111:11111:11111:11111:11111:
Db      174 SVEGTRFFDQYWSVRKSVIGSGITTTGNHFDAMARAGMLDGFQYIMATGEGYSSGS 233

OY      185 ASITVS 190
        :11111
Db      234 SNITVS 239

RESULT 38
O9KEF3
ID      09KEF3      PRELIMINARY;      PRT;      210 AA.
AC      09KEF3:
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Endo-1,4-beta-xylanhydrolase.
GN      BH0899.
OS      Bacillus halodurans.
OC      Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC      Bacillaceae; Bacillus.
OX      NCBI_TaxID=86665;
RN      [1]

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RP      SEQUENCE FROM N.A.
RC      STRAIN-C-125 / JCM 9153;
RX      MEDLINE=20512582; PubMed=11058132;
RA      Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA      Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA      Horikoshi K.;
RT      "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT      halodurans and genomic sequence comparison with Bacillus subtilis ";
RL      Nucleic Acids Res. 28:4317-4331(2000).
DR      EMBL: AP001510; BAB04618.1; -
DR      HSSP: P09850; 1XNB.
DR      InterPro: IPR001137; GH_11.
DR      Pfam: PF00457; Glyco_hydro_11; 1.
DR      PRINTS: PR00911; GLHYDLASE11.
DR      PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM      Hydrolase, complete proteome.
SQ      SEQUENCE      210 AA; 23313 MW; AC4BA5DD5D67A1B2 CRC64;

Query Match      50.5%; Score 527.3; DB 16; Length 210;
Best Local Similarity 52.5%; Pred. No. 9.7e-15;
Matches 95; Conservative 33; Mismatches 46; Indels 7; Gaps 4;

OY      14 FYSTWMDHGGVTTYTNGPGQSFVNSNSGNEFVGKGMQPGTKNKVINF-SGTYNPGNS 72
        11111:11111:11111:11111:11111:11111:11111:11111:11111:11111:
Db      31 YWQWTDGGGTVATNATNGPGCNYSVTWMDTGNFVVGKMEIGSPRTIHYNAGVWEPGNG 90

OY      73 YLSVYSGSRNPLEYIVENFGTYNPSTGATKLGCVTSDSGVYDITQRYVNOPPSITGTA 132
        11111:11111:11111:11111:11111:11111:11111:11111:11111:11111:
Db      91 YLTLYGWRNQLLEYVVDWNGYRPT--GTHRGTVSDGTYDITTYMRYNAPSIDGTQ 148

OY      133 TFEYQWSVRRNRHSSG---SVNTANHFENMAAOGLTGLG-TMDYQIVAVEGYSFGSASIT 188
        11111:11111:11111:11111:11111:11111:11111:11111:11111:11111:
Db      149 TFGQFMSVRKSRPTGNNVITFSNHNANRNGMNLGSSMSYQVLATBEGYSSGRSNVT 208

OY      189 V 189
        1
Db      209 V 209

RESULT 39
O8VP72
ID      08VP72      PRELIMINARY;      PRT;      357 AA.
AC      08VP72:
DT      01-MAR-2002 (TREMBLrel. 20, Created)
DT      01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Xylanase.
GN      XYN10D.
OS      Pseudomonas cellulosa.
OC      Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC      Pseudomonas.
OX      NCBI_TaxID=155077;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Nagy T., Fontes C.M.G.A., Ferreira L.M.A., Gilbert H.J., Emami K.;
RT      "Evidence for temporal regulation of Pseudomonas cellulosa xylanases
RT      belonging to glycoside hydrolase family 11.";
RL      Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AY065640; AAU57754.1; -
DR      InterPro: IPR001137; GH_11.
DR      Pfam: PF00457; Glyco_hydro_11; 1.
DR      PRINTS: PR00911; GLHYDLASE11.
DR      PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; UNKNOWN.1.
SQ      SEQUENCE      357 AA; 37912 MW; 42FA4BCBB29A159 CRC64;

Query Match      50.1%; Score 524; DB 2; Length 357;
Best Local Similarity 50.3%; Pred. No. 3.7e-14;
Matches 97; Conservative 41; Mismatches 45; Indels 10; Gaps 5;

OY      7 TGYNNGFYSYWMDHGGVTTYTNGPGQSFVNSNSGNEFVGKGMQPGTKNKVINFSGS 65
        11111:11111:11111:11111:11111:11111:11111:11111:11111:11111:
Db      35 TGTNNGFYTYFWKDS-GDASMTLLSGRYOSSWNSSTNNVYGKGMNPSSRVISYSGY 93

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QY 66 Y--NPNNGSYLSVYGMARNPLIEYIVENFGYVNP--TGATKLGCVTSDGSVDIYRTQ 121
 DB 94 YGVDSQSSSYLALYGMTRSPLEIYVIESYSGVSCGGDYGFSDCATYVVRRCQ 153
 QY 122 RVNQSIICTATFYGYMVRNRHRS----SGSVNANHPNMAOGLTGTNDYQIVAVE 177
 DB 154 RVNQSISGNGTIFYFYGVNRPKKFGNIGSITTFANHANFWATKGLGNHNHYOLATE 213
 QY 178 GYFSSGSASITVS 190
 DB 214 GYOSRGSSDITVS 226

RESULT 40

Q43993 PRELIMINARY: PRT: 211 AA.
 AC Q43993:
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE xylanase I precursor.
 GN XYNA.
 OS Aeromonas punctata (Aeromonas caviae).
 OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
 OC Aeromonas.
 OX NCBI_TaxID=648;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ME-1: TISSUE-GUT CONTENT OF SILK WORM;
 RA Kubota K.B., Suzuki T., Horitsu H., Kawai K., Takamizawa K.;
 RT "xylanase I of Aeromonas caviae ME-1 isolated from the intestine of a
 heterivorous insect (samia cynthia pyralis).";
 RL Biosci. Biotechnol. Blochem. 56:1463-1464(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ME-1: TISSUE-GUT CONTENT OF SILK WORM;
 RA Suzuki T., Itoh Y., Naito H., Kubota K.B., Horitsu H., Takamizawa K.,
 RA Kawai K.;
 RT "Molecular cloning of the xynA gene encoding an endo-xylanase (xylanase
 RT I) of Aeromonas caviae ME-1";
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D32065; BAA06837.1; -
 DR HSSP: P09850; IXNB.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW SIGNAL.
 FT SIGNAL 1 28 POTENTIAL.
 FT CHAIN 29 211 MATURE XYLANASE I.
 SO SEQUENCE 211 AA: 23136 MW; F9E30403EB935E49 CRC64;

Query Match 49.6%; Score 518.3; DB 2; Length 211;
 Best Local Similarity 53.6%; Pred. No. 2.3e-14;

Matches 97; Conservative 31; Mismatches 46; Indels 7; Gaps 5;

QY 14 FYSYWNDSGGVYTNPGGQFVSNWMSNGNFVGKGMQPGTKNKVINF--SGSYNPNGNS 72
 DB 32 YQMWNTOGGGTVNAVNGGNGSVSMQNTGNFVVGKGTGTTPRVVYVNGVAPSPGNG 91
 QY 73 YLSYVGSARNPLIEYIVENFGYVNPSTGATKLGCVTSDGSVDIYRTQRYNOPSIICTA 132
 DB 92 YLTFYGMTRNPLIEYIVDVDSMGTYRP--TGYTK--GTVNSDGGCTYDIYTTMRYNAPSIDGTQ 149
 QY 133 TFYQYWSVRNRHRSRG--SVNTANHPNMAOGLTGT--TNDYQIVANEGYFSSGSASIT 188
 DB 150 TFPYQYWSRKRPTGVNSTITFSNHNAMPSKGYLGNMSYQVMATEGYOSSGNANVT 209
 QY 189 V 189
 DB 210 V 210

RESULT 41

Q9ZB36

OBVVC3 PRELIMINARY: PRT: 213 AA.

AC Q9ZB36:
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Endo-xylanase.
 GN XYL.
 OS Bacillus sp. NB1420.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=165829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hong I.P., Lee S.Y., Choi S.G.;
 RT "Cloning and Expression of a Endo-xylanase Gene from Bacillus sp.
 RT NB1420 in E. Coll.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF441773; AAL32473.1; -
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; UNKNOWN_1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; UNKNOWN_1.
 KW Xylan degradation; Hydrolase; Glycosidase.
 SO SEQUENCE 213 AA: 23341 MW; 4CC0DFPF25E7551 CRC64;

Query Match 49.2%; Score 514.2; DB 2; Length 213;
 Best Local Similarity 53.8%; Pred. No. 3.5e-14;

Matches 98; Conservative 29; Mismatches 47; Indels 8; Gaps 6;

QY 14 FYSYWNDSGGVYTNPGGQFVSNWMSNGNFVGKGMQPGTKNKVINF--SGSYNPNGNS 72
 DB 33 YQMWNTOGGGTVNAVNGGNGSVSMQNTGNFVVGKGTGTSPSTIVYVNGVAPSPGNG 92
 QY 73 YLSYVGSARNPLIEYIVENFGYVNPSTGATKLGCVTSDGSVDIYRTQRYNOPSIICTA 131
 DB 93 YLALYGMTRNPLIEYIVDVDSMGTYRP--TGYTK--GTVNSDGGCTYDIYTTMRYNAPSIDOK 150
 QY 132 ATFYQYWSVRNRHRSRG--SVNTANHPNMAOGLTGT--TNDYQIVANEGYFSSGSASIT 187
 DB 151 TTFYQYWSVRNOKRPTGVNSTITFSNHNAMPSKGYLGNMSYQVMATEGYOSSGSNSV 210
 QY 188 TV 189
 DB 211 TV 212

RESULT 42

Q9ZB36

OBVVC3 PRELIMINARY: PRT: 213 AA.

AC Q9ZB36:
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Endo-1,4-beta-xylanhydrolase.
 GN XYNA.
 OS Bacillus sp.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1409;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kim S.C., Jeong K.J., Kim M.S.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U51675; AAD10834.1; -
 DR HSSP: P09850; IXNB.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.

Q8RMN9 PRELIMINARY: PRT: 213 AA.
AC Q8RMN9;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Endo-1,4-xylinase.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA Sun J., Gu S., Li W., Xu Z., Zhao H., Xiao J., Fu L.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF490979; AAM08359.1; -
KW Xylan degradation; Hydrolase; Glycosidase.
SQ SEQUENCE 213 AA; 23277 MW; 34DFAD49C2C0034 CRC64;

Query Match 46.6%; Score 487.2; DB 2; Length 213;
Best Local Similarity 52.7%; Pred. No. 4.5e-13;
Matches 96: Conservative 29; Mismatches 49; Indels 8; Gaps 6;

QY 14 FYSYNDGCHGVTTNGGQFVSVMNSGNFVGKQMPGKKNVNF-SGSYNPNGNS 72
Db 33 YWQMTDGGGIVNAVNSGSGVSNVMTGNFVVGKGTGSPERTINYNAGVMAPNGNG 92
QY 73 YLSVYGNRNPILIEYIYENFGTYNPSTGATKLGESVYDIYRTQVNPQPSITG-T 131
Db 93 YLTIXGTRSPILIEYIYVDSMGTIRP-TGYTK-GTVKSDGGTYDITTRINAPSIDDR 150
QY 132 ATFYQVWSVRNRHSSGS---VNTANHFNAMAQOGLTGT-MDYQIVAVEGFSSGSASI 187
Db 151 TTFQYGVSVQTKRPTGSNATITFSNHVDAMKSHOMNLGSMKAYVMAETEGVSSGSNV 210
QY 188 TV 189
Db 211 TV 212

RESULT 49
087118 PRELIMINARY: PRT: 457 AA.
AC 087118;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Xylanase.
GN XYNB.
OS Clostridium thermocellum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1515;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-F1;
RX MEDLINE-99239090, PubMed-10222584;
RA Hayashi H., Takehana M., Hattori T., Kimura T., Karita S., Sakka K.,
RA Ohmura K.;
DE "Nucleotide sequences of two contigations and highly homologous xylanase
genes xyna and xynb and characterization of xyna from Clostridium
thermocellum.";
RL Appl. Microbiol. Biotechnol. 51:348-357(1999).
DR EMBL: AB010958; BAA33542.1; -
DR HSSP: P36217; IXYO.
DR InterPro: IPR005084; CBM_6.
DR InterPro: IPR002105; Dockerin_1.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF03422; CBM_6; 1.
DR Pfam: PF00404; Dockerin_1; 2.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRASE11.

DR PROSITE: PS00448; CLOS_CELLULOSE_RPT; 2.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_2.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; UNKNOWN_1.
SQ SEQUENCE 457 AA; 49884 MW; 86A8C048DF12C4C5 CRC64;

Query Match 45.8%; Score 478.7; DB 2; Length 457;
Best Local Similarity 49.7%; Pred. No. 4.3e-12;
Matches 96: Conservative 26; Mismatches 58; Indels 13; Gaps 6;

QY 4 QPGTGNNGFYSTYND-GHGGVYTTNGPGQFVSVMNSGNFVGKQMPGTRKNK--- 58
Db 36 QTGTG--GGYNEFYWKDYGNG--TWVLKDGGAFCSCENINNIILFRKGFYDETRTHQOL 91
QY 59 ---VINFGSYNPNGNSYLSYVGNRNPILIEYIYENGTNPSTGATKLGESVDSGV 115
Db 92 GTITVYTCNPONNSYLSYVGNRNPILIEYIYENGTNPSTGATKLGESVDSGV 150
QY 116 DIYRTQVNPQPSITGATFYQVWSVRNRHSSGSVNTANHFNAMAQOGLTGTMDYQIVA 175
Db 151 ELEYETTRVNPQPSIKGTATFQQYWSVTRSKRTSGITSVTEHFRKAMRLGMKMKMEVALV 210
QY 176 VEGYFSSGSASIT 188
Db 211 VEGYQSSGKADVT 223

RESULT 50
052779 PRELIMINARY: PRT: 457 AA.
AC 052779;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Xylanase V.
GN XYNV.
OS Clostridium thermocellum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1515;
RN [1]
RP SEQUENCE FROM N.A.
RA Fernandes A.C., Fontes C.M.G.A., Clarke J.H., Hazlewood G.P.,
RA Gilbert H.J., Fernandes T.H., Ferreira L.M.A.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF047761; AAC04578.1; -
DR HSSP: P36217; IXYO.
DR InterPro: IPR005084; CBM_6.
DR InterPro: IPR002105; Dockerin_1.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF03422; CBM_6; 1.
DR Pfam: PF00404; Dockerin_1; 2.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRASE11.
DR PROSITE: PS00448; CLOS_CELLULOSE_RPT; 2.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_2.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; UNKNOWN_1.
SQ SEQUENCE 457 AA; 49964 MW; 637DF52A0DACF889 CRC64;

Query Match 45.7%; Score 477.9; DB 2; Length 457;
Best Local Similarity 49.5%; Pred. No. 4.6e-12;
Matches 94: Conservative 27; Mismatches 56; Indels 11; Gaps 5;

QY 7 TGYNNGFYSTYND-GHGGVYTTNGPGQFVSVMNSGNFVGKQMPGTRKNK----- 58
Db 37 TGTGCVNFEYWKDYGNG--TWVLKDGGAFCSCENINNIILFRKGFYDETRTHQOLGYI 94
QY 59 VINFGSYNPNGNSYLSYVGNRNPILIEYIYENGTNPSTGATKLGESVDSGVYDIY 118
Db 95 TVTYSNPNPNSYLSYVGNRNPILIEYIYENGTNPSTGATKLGESVDSGVYDIY 153

